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APPLICATION EXPLANT: EVALIXIS Plant Sciences, Inc.
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF AN ANTHOCYANIN MUTANT (ANT TITLE OF INVENTION: TOMATO
FILE REFERENCE: EPO1-002C
CURRENT APPLICATION NUMBER: US/10/033,190
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/244,685
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 825
TYPE: DNA
ORGANISM: Lycopersicon esculentum
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; Sequence 4, Application US/10033190
; Publication No. US20020133848A1
; GENERAL INFORMATION:
 APPLICANT: Exclixis Plant Sciences, Inc.
    TITLE OF INVENTION: IDENTIFICATION AND CHARA
    TITLE OF INVENTION: TOMATO
    CURRENT APPLICATION NUMBER: US/10/033,190
    CURRENT FILING DATE: 2001-10-29
    PRIOR APPLICATION NUMBER: US 60/244,685
    PRIOR FILING DATE: 2000-10-30
    NUMBER OF SEQ ID NOS: 5
    SOFTWARE: PatentIn version 3.1
    SEO ID NO 4
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(ANT)

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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Fang, Yiwen
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Fac
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 45
LENGTH: 1236
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US-10-021-811-45
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                                                           FEATURE:
FEATURE:
NAME/KEY: unsure
LOCATION: (519)
NAME/KEY: unsure
'``"TION: (521)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45, Application US/10021811 Publication No. US20030024007A1 GENERAL INFORMATION:
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   NAME/KEY: unsure
LOCATION: (530)..
NAME/KEY: unsure
LOCATION: (534)
                                                                                                                                                        ORGANISM: Glycine
                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               986 ATTGACTTATGGAATCTACTTGATTAA 1012
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TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
SEQ ID NO 251
LENGTH: 1300
                                                RESULT 5
US-10-021-811-43
; Sequence 43, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 23; Conserva
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; LOCATION: (168)..(1196)
; OTHER INFORMATION: G1640
US-09-934-455-251
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US-10-021-811-45
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Best Local Similarity
Matches 23; Conserv
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APPLICANT: Cahoon, Reber
APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
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LOCATION:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                     253 GGCAACAGATGGTCACTTATTGC 275
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Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
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(1124)
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(800)
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Pilgrim, Marsha
Ratcliffe, Oliver
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Yu, Guo-Liang
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o. US20030121070A1
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                                     Rebecca E.
                                                                                                                                                                                                                                                                              2.8%;
                                                                                                                                                                                                                                           Score 23; DB; Pred. No. 0.5
                                                                                                                                                                                                                                                            DB 11;
0.52;
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0.52;
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PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 43
LENGTH: 1348
Type: Num
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Otl
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT TLING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/33,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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US-09-878-574-2454
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                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                    Sequence 1, Application US/10329960 Publication No. US20030099277A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2454
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME KEY: unsure
LOCATION: (1)..(390)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-024-Q1-B1-G6
-09-878-574-2454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
              APPLICANT: Pleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P1
FULE REFERENCE: PB186P1
CURRENT FAPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR APPLICATION NUMBER: US 09/643,990
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ORGANISM: Glycine max
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FILING DATE: 2000-08-23
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larity 100.0%;
Conservative
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                           Score 21; ; Pred. No.
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0.52;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 390;
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NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
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NAME/KEY: misc feature

*COMTION: (36551)..(36551)

requal
                                                                                              FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
(47036)..(47036)
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals
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LOCATION: (9921)...(9921)
OTHER INFORMATION: n equals
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LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals
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LOCATION: (45732)...(45732)
OTHER INFORMATION: n equals
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LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals
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LOCATION: (44416)...(44416)
OTHER INFORMATION: n equals
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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LOCATION: (36636)..(36636)
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OTHER INFORMATION: n equals
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LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals
                                        LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals
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LOCATION: (45593)..(45593)
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LOCATION: (29298)..(29298)
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NAME/KEY: misc_feature
LOCATION: (51602)..(51602)
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NAME/KEY: misc_feature
LOCATION: (122167)..(122167)
OTHER_INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,
                                             NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER_INFORMATION: n equals
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals
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.OCATION: (120038)..(120038)
DTHER INFORMATION: n equals
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LOCATION: (119524)..(119924)
DTHER INFORMATION: n equals a,
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LOCATION: (119750)..(119750)
OTHER_INFORMATION: n equals
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LOCATION: (107248)...(107248)
DTHER INFORMATION: n equals a,
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
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LOCATION: (80024)..(80024)
OTHER_INFORMATION: n equals
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LOCATION: (65313)..(65313)
DTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OCATION: (117136)...(117136)
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.OCATION: (105121)..(105121)
NTHER INFORMATION: n equals a,
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THER INFORMATION: n equals
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OCATION: (100091)..(100091)
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Aun, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PL
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
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                                                                                                                                                                                                             GENERAL
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                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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LOCATION: (147197)...(147197)
OTHER INFORMATION: n equals
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LOCATION: (145942)...(145942)
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (131360) .. (131360)
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LOCATION: (150841) ..(150841)
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
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LOCATION: (152500)..(19
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9.6;
                                                                                                                                         PLANTS,
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RESULT 9
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; TYPE: DNA
; ORGANIZM: Arabidopsis thallana
US-09-938-842A-121
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SEQ ID NO 121
LENGTH: 741
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Best Local
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SEQ ID NO 121
                                     SEQ ID NO 24702
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                                                 CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                             APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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PRIOR FILING DATE: 2001-06-22
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TYPE: DNA
                  ENGTH: 1782
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APPLICATION NUMBER: US 60/264,647
FILING DATE: 2001-01-16
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100.0%; Pred. No. 17
tive 0; Mismatches
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100.0%; Pred. No.
tive 0; Mismatc
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17;
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17;
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US-10-098-263B-91990/c
Sequence 91990, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapien
US-10-098-263B-91990
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                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1,
SEQ ID NO 91990
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Best Local Similarity
Matches 20; Conserv
                   SOFTWARE: FastSEQ
SEQ ID NO 31145
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/098,263B CURRENT FILING DATE: 2003-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mittman, Michael TITLE OF INVENTION: Human Microarray
                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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                                                                                                       PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                               PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                         PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/185,218
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LENGTH: 966
                                                                                                                             FILING DATE: 1999-09-28
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18;
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US-10-027-632-31145
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
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Best Local :
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-04-20
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                                                                         PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29
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                                 APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24
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APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
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100.0%; Pre
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Search completed: January 30, 2004, 11:45:43 Job time : 327 secs

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; ORGANISM: Human
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SEQ ID NO 101162
LENGTH: 1106
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 101162
LENGTH: 1106
                                                                 Best Local Similarity
Matches 19; Conserv
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                RIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/156,358 FILING DATE: 1999-09-28
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US-09-280-590A-30

US-09-328-352-1167

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821 14 1.7 993 822 14 1.7 993 823 14 1.7 993 824 14 1.7 993 825 14 1.7 993 825 14 1.7 1000 827 14 1.7 1001 828 14 1.7 1001 829 14 1.7 1001 830 14 1.7 1001	814 1.7 993 815 14 1.7 993 816 14 1.7 993 817 14 1.7 993 818 14 1.7 993 819 14 1.7 993 820 14 1.7 993 821 14 1.7 993	800 14 1.7 993 808 14 1.7 993 809 14 1.7 993 810 14 1.7 993 811 14 1.7 993 812 14 1.7 993 813 14 1.7 993	799 14 1.7 979 800 14 1.7 989 801 14 1.7 980 802 14 1.7 987 803 14 1.7 987 804 14 1.7 990 805 14 1.7 990 805 14 1.7 990 806 14 1.7 990 807 14 1.7 990	C 786 14 1.7 949 C 787 C 788 14 1.7 949 C 788 14 1.7 949 C 789 14 1.7 951 790 14 1.7 955 C 792 14 1.7 965 C 793 14 1.7 966 C 794 14 1.7 966 C 795 14 1.7 966 C 796 14 1.7 966 C 797 14 1.7 966 C 797 14 1.7 978 C 798 14 1.7 978	C 750 C 750 C 760 C 760 C 761 14 C 763 14 765 14 766 14 767 170 14 C 772 14 C 773 14 C 778 16 C 778 17
821 14 1.7 993 2 822 14 1.7 993 2 823 14 1.7 993 2 824 14 1.7 993 2 825 14 1.7 993 4 826 14 1.7 1000 4 827 14 1.7 1001 3 828 14 1.7 1001 3 828 14 1.7 1001 4 830 14 1.7 1001 4	814 1.7 993 2 815 14 1.7 993 2 816 14 1.7 993 2 817 14 1.7 993 2 818 14 1.7 993 2 819 14 1.7 993 2 820 14 1.7 993 2 821 14 1.7 993 2	800 14 1.7 993 1 808 14 1.7 993 1 809 14 1.7 993 1 810 14 1.7 993 1 811 14 1.7 993 2 813 14 1.7 993 2	799 14 1.7 979 1 800 14 1.7 980 6 801 14 1.7 980 6 802 14 1.7 987 4 803 14 1.7 987 4 804 14 1.7 990 2 805 14 1.7 990 2 806 14 1.7 990 3 807 14 1.7 990 4	C 786 14 1.7 949 3 C 787 14 1.7 949 3 C 788 14 1.7 949 3 C 789 14 1.7 951 4 790 14 1.7 955 4 791 14 1.7 965 2 C 792 14 1.7 966 4 C 793 14 1.7 966 4 C 793 14 1.7 966 4 C 795 14 1.7 966 4 C 797 14 1.7 966 4 C 797 14 1.7 966 4 C 797 14 1.7 978 1	C 759 C 759 C 759 C 760 C 760 C 760 C 761 C 761 C 762 C 762 C 762 C 763 C 763 C 764 C 765 C 766 C 766 C 767 C 766 C 767 C 770 C 777 C 777 C 777 C 778

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11.77	1.7		1.7 1.7 1.7	1.7 1.7 1.7	1.7	1.7	11.7	1.7	1.7	1.7 1.7 1.7	1.7	1.7		11.7		1.7	1.7
1246 1246 1246 1246 1246 1246 1246	1225 1227 1229 1233 1236	1200 1200 1202 1209	1152 1158 1164 1185	1143 1146 1146 1151	1134 1140 1143	1128 1128 1128 1131	1110	1098 1101 1103 1103	1072 1072 1083 1086	1072 1072 1072 1072	1071	1059 1059 1070	1053	1034	1024 1026 1032	1008	1002
1 US-08-741-134-5 1 US-08-997-828-2 1 US-08-480-756-2 2 US-08-462-403-2 4 US-09-651-656-30 4 US-09-650-855-30 5 PCT-US93-10419-2 3 US-08-910-505-3	US-09-5 US-09-1 US-08-2 US-09-6 US-08-3	US-09-1 US-09-6 US-09-3 US-09-3	US-09-3 US-09-3 US-09-1 US-09-1	US-09-3 US-09-1 US-09-3 US-09-4	US-09-5 US-09-2 US-09-3	US-09-4 US-09-6 US-09-3	US-08-8 US-09-2 US-09-3	US-09-0 US-09-2 US-09-1 US-08-5 US-09-3	US-08-4 PCT-US9 US-09-1 US-09-1	US-08-4 US-08-4 US-08-4 US-08-4	US-09-2 US-07-9 US-08-4	US-08-7 US-09-5 US-08-1	US-08-9 US-09-3	US-09-107-532A-305 US-09-363-970-35 US-09-221-017B-555	US-09-3 US-09-3 US-09-1	US-09-3 US-09-3	US-09-6 US-08-9 US-09-2
sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 30, Appl Sequence 30, Appli Sequence 3, Appli	equence 99 equence 25, equence 1, equence 49; equence 7, equence 5.	equence 62: equence 38: equence 97 equence 24 equence 49	equence 18 equence 15 equence 78 equence 29	equence 21: equence 19: equence 22: equence 63	equence 2, equence 53 equence 15	equence 12 equence 10 equence 10 equence 25	equence 2, equence 71: equence 33:	equence 39 equence 15 equence 36 equence 4, equence 33	equence 5, equence 5, equence 86 equence 12	equence 5, equence 5, equence 5, equence 5,	equence 5, equence 5,	equence 3, equence 8, equence 17	equence 1, equence 1, equence 60	equence 35 equence 55 equence 55	equence 66 equence 32 equence 26	equence 3, equence 3, equence 64 equence 64	equence 59 equence 3, equence 3,
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Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
APPLICANT: Fleischmann et al.
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   986
988
989
                                                                             TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOPTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «UDKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Michalle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
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ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                    APPLICATION NUMBER: 08/476,102 FILING DATE: JUN-5-1995
                                                                                                                                                                                                                                                                                                                                                                                             STATE: MD
                          TOPOLOGY: linear
                                                    TYPE: nucleic acid
                                                                                                                      TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
                                                                  LENGTH: 1830121 base pairs
              DESCRIPTION: SEQ ID NO:
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US-09-134-001C-989
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US-09-252-991A-11439
US-08-660-347-1
US-08-413-574-1
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US-08-185-828A-22
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1653, Ap
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1824, Ap
11439, A
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22, Appl
218, App
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2, Appli
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RESULT 3
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US-09-643-990A-1/c
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GENERAL INFORMATION:
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Best Local S
                                                                     Matches
                                                                                                    Query Match
                                                                                                                                                                                                                                        TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVEY
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P10
TELECOMMUNICATION INFORMATION:
                                                         2.5%;
Local Similarity 100.0%;
hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
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                                   788
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TITCIGCIGAAATIGACITAI 808
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TITCIGCIGAAATIGACTIAI 1174308
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                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Craig Venter
OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                        LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mark D. Adams
Owen White
Hamilton O. Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 1/2 inch diskette
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pred. No. 0.5
nismatches
                                                                    0;
                                                                                     Score 21; DB 4;
Pred. No. 0.54;
                                                                     Mismatches
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0.54;
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Query Match
Best Local Similarity
Watches 19; Conserve
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US-09-212-247C-1/c
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GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09212247C Patent No. 6391603
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (608) 2: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                             APPLICANT: POMPEJUS, Markus; SUELBERGER, Harald; JOEFFKEN, Hans Wolfgang; DOVAL, Jose Luis Revuelta; JIMENEZ, Alberto; and GARCIA, Maria Angeles Santos
TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the use thereof in microbial riboflavin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                   612 GGTTCATGGACTGATGAAG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 GGTTCATGGACTGATGAAG 58
STATE: D.C.
COUNTRY: USA
ZIP: 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.3%; Score 19; DB 4; ilarity 100.0%; Pred. No. 7.5; Conservative 0; Mismatches
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Parna, Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plunkett, Guy
Welch, Rod
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CURRENT APPLICATION NUMBER: US/09/699,266A
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: PC/US99/08385
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/083,212
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 999
TYPE: DNA
ORGANISM: Triticum aestivum
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-212-247C-1
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                                    Matches
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                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ma, Hongchang
APPLICANT: Morakinyo, Layo O.
APPLICANT: Odell Joan T.
APPLICANT: Orozeco Jr., Emil |
                                                                                                                                                                                                                                                                                                                        APPLICANT: Orozsco Jr., Emil M.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: TRANSCRIPTION AND GENE EXPRESSION REGULATORS
FILE REFERENCE: BB1164 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS;
                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1911 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/212,247C
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   598 ATTGAAGAAGATGAAGAG 615
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                                                    Similarity
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LOCATION:
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                                   Conservative
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626..1582
                                                  2.2%;
                                                  Score 18; Pred. No.
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                                                    DB 4;
23;
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                                                                Length 999;
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LENGTH: 1033
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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CURRENT APPLICATION NUMBER: US/09/610,185C
CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: US 09/603,244
PRIOR PILING DATE: 2000-6-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                             TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Borevitz, Justin
APPLICANT: Xia, Yiji
APPLICANT: Dixon, Richard i
APPLICANT: Lamb, Christoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201.487-5800
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/928,941D FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hirai, Hiroshi
APPLICANT: Sherr, Charles
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 2.2%; Score 18;
Local Similarity 100.0%; Pred. No.
es 18; Conservative 0; Mismatch
                                                                                                                                                                                                            CLASSIFICATION: 435
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  ENGTH:
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Lamb, Christopher J.
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3767 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Continental Plaza,
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; ORGANISM: Hon
US-08-928-941D-30
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                                                          Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                  TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3767 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGIE TYPE: CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hirai, APPLICANT: Sherr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                 TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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2620 TGAAGAGGTTGTAATTAA 2603
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                             609 TGAAGAGGTTGTAATTAA 626
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                                                                                                                                                                                                                  nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                   3767 base pairs
                                                                                                                                                                                                                                                                                                  201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                          Conservative
                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                     linear
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                                                                           100.0%;
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                                                                            Score 18; ; Pred. No.
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                                                            Mismatches
                                                                            DB 3;
21;
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                                                                                           Length 3767;
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RESULT 9 US-09-280-590A-28/c

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RESULT 10
US-09-280-590A-30/c
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                                                                                                                                                                                                                         Sequence 30, Application US/09280590A Patent No. 6303772 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/09280590A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.2%;
Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/280,590A
FILING DATE: 29-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
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TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hirai, Hiroshi
                                                                                                            TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES THEREOF
                                                                                                                                                                                                       APPLICANT: Hirai, Hiroshi
                                                                                            NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                 609 TGAAGAGGTTGTAATTAA 626
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CITY: Hackensack
                                 STREET: 411 Hackensack Ave, Continental Plaza, 4th
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LENGTH: 3767 base pairs
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                                                                                                                                                                 Charles
Kazushi
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                                                                                                                                                    Sarah M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                   RESULT 12
US-08-926-842B-11/c
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-1695
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                 Sequence 11, Application US/08926842B Patent No. 6030807
                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 18; Conserv
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SEQ ID NO 1695
LENGTH: 7515
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/280,590A
FILING DATE: 29-Mar-1999
CLASSIFICATION: «Uhknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PC-BOS/MS-DOS CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: RNA
                                                                                                                                  5008 AAGTTAAATACTACTAAA 5025
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                                                                                                                                                            340 AAGTTAAATACTACTAAA 357
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STRANDEDNESS: single
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                                                                                                                                                                                                           Conservative
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Pred. No.
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                                                                                                                                                                                                           Mismatches
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21;
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE: OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-487-5800
TELEPAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
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                                       Length 7515;
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  Indels
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Gaps
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FEATURE:
NAME/KEY:
LOCATION:
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WFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DI
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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NAME/KEY:
                           OTHER INFORMATION:
                                                                                      OTHER INFORMATION: /product= "araP'
                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                        LOCATION: 4107..4916
OTHER INFORMATION: /product= "araL"
                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /product=
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OTHER INFORMATION:
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REFERENCE/DOCKET NUMBER: 600-1-089 N
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                                                         NAME/KEY:
                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 10917 base pairs
TYPE: nucleic acid
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                                            LOCATION:
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New Jersey
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                                            8407..9255
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                           /product= "araQ"
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GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 1167

LENGTH: 750

TYPE: DNA

ORGANISM: Acinetobacter baumannii

US-09-328-352-1167
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US-09-328-352-1167
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CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 3555
LENGTH: 271
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Best Local Similarity
Matches 18; Conserv
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APPLICANT: Lalgudi
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Patent No. 647621
                                                             Matches
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NAME/KEY: misc_feature
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LOCATION: 166-184
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/ENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
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15278.607 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AF146702	RESULT 1
Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.,	1 (bases 1 to 1034)	Asteridae; lamiids; Solanales; Solanaceae; Petunia.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Petunia x hybrida	Petunia x hybrida		AF146702.1 GI:7673083	CCB. AF146702	Petunia x hybrida An2 protein (an2) mRNA, an2-V26 allele, complete	AF146702 1034 bp mRNA linear PLN 01-MAY-2000		

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JOURNAL
MEDLINE
PUBMED
REFERENCE
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Molecular analysis of the anthocyanin2
in the evolution of flower color
Plant Cell 11 (8), 1433-1444 (1999)
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AGGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTT
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                                                                                                                      AACGATGTCAAAAACTATTGGAACACCCACCTTCGAAAGAAGTTAATTGCTCCTCA----
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/protein_id="AAF66727.1"
/db_xref="GI:7673084"
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chromosome="6"
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AF146704
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JOURNAL
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MEDLINE
Query Match
Best Local Similarity
Matches 429; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petunia integrifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 866)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete cds.
AF146704
                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-APR-1999)
1087, Amsterdam 1081HV,
                                                                                                                                                                                                                                                                                                                                                                                                       Quattrocchio, F., W. Mol, J. and Koes, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99380006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Cell 11 (8), 1433-1444 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular analysis of the anthocyanin2 in the evolution of flower color
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quattrocchio, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petunia integrifolia
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Petunia integrifolia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANACCTCGTCCTCGGACCTTCTCAAGGCCGGCAATGAATAATTTTCCTTGTTGGAACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACTGGAAAATTGCAATGACGATATTGAAGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTGATGAGAAGCAAAAACCCGGAAGAATCGATAGATGGACTTCAATGGTGGGCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                           149578
(bases 1 to 866)
(bases 1, to 866)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. and Koes, R.
                                                              310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GTGAGAAACAAACTCCAGATGCATCGATGGACAACGTAGATCCATGGTGGATAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----CAATAATGTAATTTTGGACGAGGAGGAACATTGCAAGGAAATAATAA----
                                                   organism="Petunia
/mol_type="mRNA"
/cultivar="S6"
                                                                                                                                                                                                                                                  'gene="anz"
                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                    note="anthocyanin
                                                                                                                                                                                                                 gene="an2"
                                                                                                                                                                                                                                         allele="an2-S6"
                                                                                                                                                                                                                                                                 tissue_type="petal limb"
                                                                                                                                                                                                                                                                                          db_xref="taxon:4103"
chromosome="6"
                                                                                                                                                                              codon_start=1
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           31.7%;
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 Score 261.6; DB 8
Pred. No. 1.5e-41;
D; Mismatches 174
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protein
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E
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AF146706
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                                                                                                                                                                                                                                                                            Petunia x hybrida

Petunia x hybrida

Retunia x hybrida

Bukaryota, Viridiplantae, Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu

Asteridae; lamids, Solanales, Solanaceae; Petunia.

1 (bases 1 to 868)

Quattrocchio, F., Wing, J., van der Woude, K., Souer, E.,

Mol, J. and Koes, R.
Submitted (29-APR-1999) Generation (29-APR-1999) Generation (1981) Netheration (2011) Amsterdam (2011) Generation (2011)
                                                                     Quattrocchio, F., W. Mol, J. and Koes, R. Direct Submission
                                                                                                                                                                                                               Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
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Petunia x hybrida
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An2 truncated
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Netherlands
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                                                                                                                   Woude, K.,
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(an2) mRNA,
                                                                                                                                                                                                                                                                of petunia
                                                                                                                      Souer,
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                                                                                                                                                                                                                                                                                                                                                                                    eudicots;
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                                                                                                                      Vetten,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGGAAAAATGGCATCTTGTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGAACAGTACATCTATGTCTTCATTGGGAGGGAGAAAAGGTTCATGGACTGATGAAGAA
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    TTACTGGAAAATTGCAATGACGATATTGAAGAAGATGAAG
                                                                                                                                                                                                                                                                                                                                   CAGAAACAAGAGCAAGAGCTAGCAAAGCCATGAAA--ATCACCGAGAACAACATAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGATGTGAAAAACTATTGGAACACTAATCTTCTAAGGAAGTTAAATACTACTAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATAAGCTCTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCT
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                                                 ACTGATGAGAAGCCAAAAACCGGAAGATTCGATAGATGGACGTCAATGGTGGGCCAAT
                                                                                                                                               AAAAGTTGTAATAAAAACACTATAGACAAGAATGAAGGTGACACAGAAATAATAAAGTTT
                                                                                                                                                                                                                                                                                         AAACCTCAACGACGCAAGTATTTCTCAAGCACAATGAAGAATGTT-------
                                                                                                                                                                                                                                                                                                                                                                                 GTTCCTCGCGAAAAGATTAACAATAAGTGTGGAGAAATTAGTACTAAGATTGAAATTATA
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                                                                                 ----GTGAGAAACAAACTCCAGATGCATCGATGGACAACGTAGATCCATGGTGGATAAAT
                                                                                                                                                                                                                                            AAACCTCGTCCTCGGACCTTCTCAAGGCCGGCAATGAATCATGTTTCTTGTTGGAACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGATGTCAAAAACTATTGGAACACGCACCTTCGAAAGAAGTTAATTGCTCCTCATGAT
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                                                                                                                                                                          -ACAAACAATAATGTAATTTTGGACGAGGAGGAACATTGCAAGGAAATAATAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSTSNASTSGVRKGAWTEEEDLLLRECIDKYGEGKWHLVPVRAG
LNRCRKSCRLRWLNYLRPHIKRGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGRTAND
VKNYWNTHLRKKLIAPHDQKQESKS"
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/replace="nnnn"
140 c 191 g 227 t
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/protein_id="AAF66731.1"
/db_xref="GI:7673092"
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/chromosome="6"
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/cultivar="W22"
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/organism="Petunia x hybrida"
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Pred. No. 2.2e-41;
0; Mismatches 182;
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Best Local
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121
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Submitted (29-APR-1999) Genetics, V.
1087, Amsterdam 1081HV, Netherlands
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Quattrocchio, F., Wi
Mol, J. and Koes, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asteridae; lamiids; Solanales; Solanaceae; Petunia.
1 (bases 1 to 868)
Quattrocchio, F., Wing, J., van der Woude, K., Souer, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular analysis of the anthocyanin2 gene in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petunia x hybrida
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                                                  GATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATTAGCCAACAACATTGAGATTAAGGACTTAGCTAATG
ATAAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTA 180
                                                                                               ATGAGTACTTCTAATGCATCAACATCAGGAGTAAGGAAAGGTGCATGGACCGAGGAAGAA
                                                                                                               ATGAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAA
                                GATCTTTTATTGAGAGAATGCATTGAGAAGTATGGAGAAGGGAAGTGGCATCTAGTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L, J. and Koes, R.
                                                                                                                                                                                                                                               307
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="An2 truncated protein"
/protein_id="AAP66732.1"
/protein_id="AAP66732.1"
/db_xref="G1:7673094"
/txanslation="MSTSNASTSGVRKGAWTEBEDLLLRECIEKYGEGKWHLVPVRAGLARCKSCRLRWLNYLRPHIKRGDFSLDEVELILRLHKLLGNRWSLIAGRLPGRTAND
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                                                                                                                                                                                                                                                                                           gene="an2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="anthocyanin regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'tissue_type="petal limb"
.. .868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:4102"
chromosome="6"
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                                                                                                                                                                                                                                                                          note="causes frameshift leading
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An2 truncated
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Pred. No. 2.2e-41;
0; Mismatches 182;
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protein
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Petunia integrifolia

Petunia integrifolia

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 865)

Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.,

Quattrocchio, F., Wing, J., van der Woude, K.,
                                                                                                                                                                                                                                                                             Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999) 99380006
                                                                                                                                                               Submitted (29-APR-1999) Genetics, Vrije Universiteit, 1087, Amsterdam 1081HV, Netherlands
                                                                                                                                                                                            2 (bases 1 to 865)
Quattrocchio, F., Wing, J.,
Mol, J. and Koes, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete cds.
                                                                                                                                                                                                                                                                                                                                              Mol,J. and Koes,R.
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                                                                                               /mol
                /tissue_type="petal limb"
1. .865
/gene="an2"
                                               /db_xref="taxon:4103"
/chromosome="6"
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AF146705 909 bp Petunia x hybrida An2 truncated allele, complete cds. AF146705 AF146705.1 GI:7673089
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133 c 193 g 229 t 1 others
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12. .77°
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/db_xref="GI:7673086"
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/product="An2 protein"
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1 (bases 1 to 909)
Quattrocchio, F., Wing, J., van der Woude, K., Souer, E
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Quattrocchio, F., Wi
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                                                  CATAAGCTCTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCT 300
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/note="causes:
/replace=""
a 137 c 1:
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/product="An2 truncated protein"
/protein id="An2 truncated protein"
/protein id="An2 truncated protein"
/protein id="An2 truncated protein"
/db_xref="GI:7673090"
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LNRCRKSCRLEWMLVLREPHIKRGDFSLDEVELILRLHKLLGNRWSLIAGRLPGRTAND
VKNYWNTHLRKKLIVPHDQKQESKTKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="anthocyanin regulator; myb-related transcription
factor"
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/chromosome="6"
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1 (bases 1 to 865)

Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.
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Petunia axillaris
                                                                                                                                                                                                                                                                                           Submitted (29-APR-1999) Genetics, V 1087, Amsterdam 1081HV, Netherlands
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                                                                                                                          /gene="an2"
/allele="an2
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/codon_start=1
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                                                                               ractor"
                                                                                                                                                                                                         /cultivar="87"
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                                                                                                note="anthocyanin"
                                                                                                           'gene="an2"
                                                                                                                                                                  tissue_type="petal limb" . .865
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/chromosome="6"
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Submitted (29-APR-1999) Genetics, V.
1087, Amsterdam 1081HV, Netherlands
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 858)

Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
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                                                 CATAAGCTCTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCT
                                                                                                            AGGCCACATATCAAGAGAGGGGGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTT
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Myb-related genes of the Kyoho
anthocyanin biosynthesis
Planta_215 (6), 924-933 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-OCT-2001) Shozo Kobayashi, National Institute of Fruit Tree Science, Department of Grape and Persimmon Research; 301-2, Akitsu, Toyota-gun, Hiroshima 729-2494, Japan (E-mail:skobaya@affrc.go.jp, Tel:81-846-45-4719,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids; Vitaceae; Vitis.
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Vitis labrusca x Vitis vinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAAACAAGAGAGACAAAGCCATG-----AAAATTACCGAGAACAACATAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 920)
/trānslation="meslgyrkgamiqeedyllrkCiekygegkwhlyplraglnrcr
kscrlrwlnylkpdikrgefaldeydlmirlhnllgnrwsliagrlpgrtandyknyw
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/db_xref="GI:22266661"
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/function="activate the Kyoho UFGT
/note="anthocyanin regulator"
                                                                                                                                                                   /gene="VlmybA1-1"
15. .767
                                                                                                                                                                                                                                                  /cultivar="Kyoho"
/db_xref="taxon:105599"
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                                                                                                                                                                                                                /dev_stage="mature"
/tissue_lib="Uni-ZAP'
                                                                                                                                                                                                                                                                                                                             organism="Vitis labrusca"
                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                               type="mRNA"
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(yoho grape (
                                                                                                                                                                                                                      berry cDNA"
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                                                                        factor VlMYBA1-1"
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ACCESSION
VERSION
KEYWORDS
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AUTHORS
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                                                                                                                                 Direct Submission
Submitted (15-OCT-2001) Shozo Kobayashi, National Institute of Fruit Tree Science, Department of Grape and Persimmon Research; 301-2, Akitsu, Toyota-gun, Hiroshima 729-2494, Japan (E-mail:skobaya@affrc.go.jp, Tel:81-846-45-4719,
                                                                                                                                                                                                                                                                                                                     Vitis labrusca x Vitis vinifera Vitis labrusca x Vitis vinifera Eukaryota, Viridiplantae, Strens Spermatophyta, Magnoliophyta, et rosids, Vitaceae, Vitis.
                                                                                                                                                                                                                                                      Kobayashi,S., Ishimaru,M., Hiraoka,K. Myb-related genes of the Kyoho grape anthocyanin biosynthesis planta 215 (6), 924-933 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                  AB073013
Vitis labrusca
                                                                                                                                                                                                                                                                                                                                                                                                             transcription AB073013
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Kobayashi,S.
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SSKPSSTSPQPNDDIIWMESLLAEHAQNDQETDFSASGEMLIASLRAEETATQKKGPM
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165 c 210 g 233 t
 /tissue_lib="Uni-ZAP berry
1. .1173
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/mol_type="mRNA"
                                                                                                              Location/Qualifiers
                         dev_stage="mature"
                                    tissue_type="berry"
                                                  db_xref="taxon:105599"
                                                             cultivar="Kyoho"
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a x Vitis vinifera VlmybA2 gene
factor V1MYBA2, complete cds.
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                                                                                         Vitis vinifera"
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Kobayashi,S.
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10. .933
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Direct Submission
Submitted (15-OCT-2001) Shozo Kobayashi, National Institute
Fruit Tree Science, Department of Grape and Persimmon Reseas
301-2, Akitsu, Toyota-gun, Hiroshima 729-2494, Japan
                                                                                                                                                                                                                                                                                                                                                                     Vitis labrusca x Vitis vinifera
Vitis labrusca x Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB073012 903 bp. Vitis labrusca x Vitis vinifera transcription factor VlMYBA1-2,
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Myb-related genes of the Kyoho
anthocyanin biosynthesis
Planta 215 (6), 924-933 (2002)
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/note="anthocyanin regulator"
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Pred. No. 1.6e-29;
0; Mismatches 81
                                                                                                                                                                                                                                                               Hiraoka,K.
(yoho grape (
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 420)
Stracke,R., Werber,M. and Weisshaar,B.
                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                         complete cds.
AY008379
                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                          AY008379
                                                    Spermatophyta; Magnoliophyta;
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                                                                                                                                                                                                                                                                                                                                                                                   GGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATC
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/protein_id="BAC07539 1"
/protein_id="BAC07539 1"
/db_xref="G1:2266665"
/translation="MESLGVRKQAWIOEEDVLLRKCIEKYGEGKWHLVPLRAGLNRCR
KSCRLRWLNYLKPDIKRGEFALDEVDLMIRLHNLLGNRWSLIAGRLPGRTANDVKNYW
HGHHLKKKVQFOGEGRNKPLTHSKTKALKPHPHKFSKALPRFELKTTAUDTFDTQVST
SSKPSSTSPQPNDDIIWESSLIAELDQETDFSASGEMLIASLRAEETATQKKGPMDGM
IEQIQGEGDFPDVGFMDTPNTQVNHLI"
a 168 c 205 g 222 t
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/note="anthocyanin regulator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Kyoho"
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                                                                                                                                       GI:11641123
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TITLE
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Arabidopsis thaliana production
(PAP2) mRNA, complete cds.
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                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zuechtungsforschung, Carı-von
Location/Qualifiers
Borevitz,J.O., Xia,Y., Blount,J., Dixon,R.A. and Lamb,C. Activation tagging identifies a conserved MYB regulator of
                 1 (bases 1 to 992)
Borevitz, J.O., Xia, Y.,
                                                                                                  Arabidopsis thaliana
                                                                                                                                                     AF325124
AF325124.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-SEP-2000) Dept. Biochemie, Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln D-50829, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 420)
Stracke, R. and Weisshaar, B.
                                                                                                                    Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                           TEGAACACCCATCTGAGTAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEGSSKCLRKCAMTAEEDSLLRQCIGKYCEGKWHQVPLRACINR
CRKSCRLRWLNYLKPSIKRGKFSSDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKN
YWNTHLSKKHEPCCKTKIKRINIITPPNTPAQKVDIF"
67 c 105 g 114 t
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/db_xref="GI:11641124"
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/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="1"
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                                                                                                                                                       GI:11935172
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Arabidopsis thaliana (thale cress)
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CRKSCRLRWLNYLKPSIKRGRLSNDEVDLLLRLHKLLGNRWSLLAGRLPGRTANDVKN
YMNTHLSKKHESSCCKSKMKKKNIISPPTFVQKLIGVFKPRPRSFSVNNGCSHLNGLP
EVDLIPSCLGLKKNNVCENSITCNDEKDDFVNNLMNGDNMMLENLLGENQEADAIV
PEATTAEHGATLAFDVEQLWSLFDGETVELD"
153 c 221 g 310 t
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/product="production of anthocyanin pigment
/protein_id="AAG42002.1"
/db_xref="GI:11935173"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="synonyms: T27F4.14,
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'chromosome="1"
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'cultivar="Columbia-0"
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Pred. No. 1.1e-26;
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2 (bases 1 to 1033)
Greco,R., Petroni,K. and Tonelli,C.
Direct Submission
Submitted (04-MAY-1998) Abt. Biochemie,
                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1033)

1 (bases 1 to 1033)

1 (bases 1, Denekamp, M., Greco, R., Jin, H., Leyva, A., Meissner, R.C., Petroni, K., Urzainqui, A., Bevan, M., Martin, C., Smeekens, S., Tonelli, C., Paz-Ares, J. and Weisshaar, B.
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAAACTAT 318
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
_161 c 226 g 31
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(MYB90) mRNA,
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Search completed: January 30, 2004, 07:56:37 Job time : 2218 secs
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Best Local Similarity 74.5%;
Matches 234; Conservative
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                                                                                                                                                                     362 AGGTGGTCCTTGATTGCTGGATTGCCTGGTCGGACCGCTAATGATGTCAAAAATTAC 421
                                                                                                                                                                                                                                                         302 GGAAGACTTAGCAATGATGATGTTGATCTTCTTCGTCGTCATAAGCTTCTAGGAAAT
                                                                                    422
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                                                                                                                                                                                                               259
                                                                                                                                                                                                                                                                                                   199 GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC 258
                                                                                                                                                                                                                                                                                                                                             242 CGATGCAGAAAGAGTTGTAGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                     139 AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                 182 TGTATTGATAAGTATGGAGAAGGCAAATGGCATCAAGTTCCTTTGAGAGCTGGGCTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 TCGTCCAAAGGGTTGÁGGÁÁAGGTGCÁTGGACTGCTGÁÁGÁAGATAGTCTCTTGAGGCTÁ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carl-von-Linne-Weg 10, Koeln D-50829, Germany Location/Qualifiers
                                                                                 TGGAACACCCATCT 435
                                                                                                                         TGGAACACTAATCT 332
                                                                                                                                                                                                      AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTAT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MEGSSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNR CRKSCRLRWLNYLKPSIKGRLSNDEVDLLLRLHKLLGNRWSLLAGRLPGRTANDVKN YWNTHLSKKHESSCCKSKMKKKNIISPTTPVQKIGVFKPRPRSFSVNNGCSHLNGLPEVDLIPSCLGLKKNNVCRNSITCNKDEKDDFVNNLMNGDNMMLENLLGENQEADAIVPEATTZEHGATLAFDVEQLWSLFDGETVELD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MYB90; R2R3-MYB factor family member"
/codon_start=1
/product="putative transcription factor"
/protein_id="AAC83637.1"
/db_xref="GI:3941522"
/db_xref="GI:3941522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="Columbia"
/db_xref="taxon:3702"
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Compugen Ltd

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                  C
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                  825
618
189.6
189.6
186
                                                                                                                                                                                                                                                                                            Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                         Match Length DB
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1: /SIDS1/gcgdata/g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:

SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:

SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:

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      ABQ73046
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ABN98500
AAD05751
ABK65155
ABK14222
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Tomato anthocyanin
Tomato anthocyanin
Arabidopsis thalia
Arabidopsis cDNA e
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis cDNA e
A. thaliana Produc
                                                                                                                                                                                                                                                                                      Description
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		21	1203	16.3	134.6	<b>4</b> 5	
		24	452	•	135.4	44	
Myb-related transc	ABT08114	24	1236	٠	135.8	43	
	AAD06651	22	1082	•	136.2	42	
Arabidopsis thalia	AAC47	21	1392	•	138	41	
	AAC49321	21	1329	16.7	138	40	
Nucleotide sequenc	AAF84746	22	1310		138	39	
		21	1280	16.7	138	38	
Arabidopsis thalia		24	960	•	138	37	
		21	373		138	36	
Arabidopsis cDNA e		24	660		138.6	35	
	AAC40461	21	1332		139.6	34	
Arabidopsis thalia	AAD06466	22	918	•	143	ω ω	
		21	839		143	32	
Arabidopsis thalia		24	810		143	31	
Arabidopsis cDNA e		24	612	•	143.4	30	
Cotton transcripti	AAF90596	22	1081	•	143.8	29	
Cotton transcripti		22	1006		143.8	28	
		22	1151	•	144.4	27	
		21	639		146.8	26	
		21	871	•	147	25	
Arabidopsis thalia		21	868	•	147	24	
CD.		24	791	٠	147	c 23	
		22	764		147	22	
Nucleotide sequenc		22	933	18.5	153	21	
Pinus radiata tran		21	504		153.2	20	
		24	774	•	154.8	19	
thali		21	774	•	154.8	18	
Myb-related transc		24	514		157.4	17	
Human GDP-mannose	ABX20395	25	390		170.6	16	
		24	925		179	15	
	ABZ1482	24	747	•	179	14	
		24	956	•	180.2	13	
Arabidopsis cDNA e		24	741	•	185.4	12	
	AAD0576	22	741	22.5	185.4	11	
	AAF851	22	1043	•	186	10	
Arabidopsis thalia	AAD47497	25	1033	•	186	9	

## ALIGNMENTS

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RESULT 1
AND073046
ID 38067
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Conners K, Mathews HV, Liu A;
                                                                                                                                                                                                          30-OCT-2000; 2000US-244685P.
                                                                                                                                                                                                                                                                                                                29-OCT-2001; 2001WO-US50638.
                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200255658-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tomato; ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tomato anthocyanin 1 (ANT1) encoding cDNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-2002 (first entry)
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                                                                                                     (EXEL-) EXELIXIS PLANT SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "anthocyanin mutant (ANT1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= a
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Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes tomato anthocyanin 1 (ANT1). The ANT1 polynucleotide can be used for modifying the expression of a native plant gene, particularly for producing an anthocyanin 1 phenotype in plants, which is responsible for many red and blue colours in plants. The polynucleotide is useful for modifying e.g. leaf colour, flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide derived from tomato, useful for producing an Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf color, flower color or fruit color in plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 200
P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colour or fruit colour in plants.
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DB; ABB81626.
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CATGAAAATTGGGGTGAATTTTCTCTTAATTTACCACCCATGCAACAAGGAGTACAAAAT
                                                                           GAAATATCACCACCACTAAAATATTGGTGAAGGTAACTCCATGCAACAAGGACAAATAAGT
                                                                                                                                                     GAAGAAGATGAAGAGGTTGTAATTAATTATGAAAAAACACTAACAAGTTTGTTACATGAA
                                                                                                                                                                                                                                                                                                                                                                                   AACGATGTGAAAAACTATTGGAACACTAATCTTCTAAGGAAGTTAAATACTACTAAAATT
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                                                        GAAATATCACCACCATTAAATATTGGTGAAGGTAACTCCATGCAACAAGGACAAATAAGT
                                                                                                                                GAAGAAGATGAAGAGGTTGTAATTAATTATGAAAAAACACTAACAAGTTTGTTACATGAA
                                                                                                                                                                                                                             TCGATGGACAACGTAGATCCATGGTGGATAAATTTACTGGAAAATTGCAATGACGATATT
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                                                                                                                                                                                                         TCGATGGACAACGTAGATCCATGGTGGATAAATTTACTGGAAAATTGCAATGACGATATT
                                                                                                                                                                                                                                                                               AGGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTT
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ilarity 100.0%;
Conservative 0
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Pred. No. 5.1e-193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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XX ABQ7
XX Toma
XX Toma
XX Toma
XX Iyco
PN W020
XX Iyco
PF 29-0
XX EXT
XX WPF COIN
XX WPI;
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                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                          The present invention describes tomato anthocyanin 1 (ANT1). The ANT1 polynucleotide can be used for modifying the expression of a native plant gene, particularly for producing an anthocyanin 1 phenotype in plants, which is responsible for many red and blue colours, flower the polynucleotide is useful for modifying e.g. leaf colour, flower colour or fruit colour in plants. The present sequence represents an ANT1 genomic DNA fragment which is used in an example from the present ANT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide derived from tomato, useful an Anthocyanin 1 phenotype in plants, particularly for leaf color, flower color or fruit color in plants -
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-OCT-2000; 2000US-244685P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tomato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato anthocyanin 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-2001; 2001WO-US50638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum
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                                                                                                                            GATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGGAAAAATGGCATCTTGTTCCC
                                                                                                                                                                                ATGAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGATTTTTCTGCTGAAATTGACTTATGGAATCTACTTGATTAA
                                                                                  ATAAGAGCT-----
                                                                                                                                                                      ATGAACAGTACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAA
                                                                                                                                                                                                                                                                                     1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGAAAATTGGGGTGAATTTTCTCTTAATTTACCACCCATGCAACAAGGAGTACAAAAT
 TTTTATTTGACGTTATTACGAATATCATCTGAAAATGTACGTGCAGGTCTGAATAGATGT
                                                       ATAAGAGCTGGTAACTATTAAATTAACTATCACGTTATTTTTATTTGTCTTTCTGTCTCA
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Pred. No. 3.9e-142;
D; Mismatches 0;
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                                                                                                                                                                                                                                                        Length 1012;
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RESULT 3
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AC AAD0
XX AAD0
DT 31-J
DT Arah
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KW Tran
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                                                                                                                                                                                                     Transcription factor; trait modification; seed characteristic; structural characteristic; developmental characteristic; gene
                                                                                                                                Arabidopsis
                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD05768 standard; cDNA;
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                                                                                                                                                                                  biotechnology;
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                          Location/Qualifiers
/product= "Transcription factor homologue G2421"
                                                                                                                                                                                                                                                                                       transcription factor homologue G2421 cDNA
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259 190 199 130 139 70 79 10 19 240;

AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAAACTAT

AGGTGGTCCTTGATTGCTGGTCGATTACCTGGTCGGACCGCTAATGATGTCAAGAACTAC

309 318 249 258 189 S

AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA

198

129

GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC CGGTGCAGGAAAAGTTGTAGACTAAGATGGTTAAAACTATTTGAAGCCAAGTATCAAGAGA

GGAAAATTTAGTTCTGATGAAGTTGATCTTCTTCTTCGTCTTCATAAGCTTCTAGGAAAT

TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT

TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA

TCGTCCAAAGGGTTGAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGCAG

69 78

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밁 8

Query Match Best Local Similarity

23.0%;

Score 189.6; DB Pred. No. 6.5e-37 0; Mismatches 8

22;

Length

0,

Matches

Conservative

0

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The present cDNA sequence is homologue G2421 of Arabidopsis thaliana transcription factor G663. The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify the to alter seed characteristics such as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits.
                                                                                                                                                                                                                                                                                    Nucleic acids encoding plant transcription factor polypeptides, for altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants -
Sequence 762 BP; 225 A; 109 C; 193 G; 235 T; 0 other;
                                                                                                                                                                                                                                                          Claim 4; Page 115; 133pp; English
                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                             Reuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CREE/)
(PILG/)
(RIEC/)
(JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-1999; 99US-0166228.
17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200135727-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YUGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-2000; 2000WO-US31457
                                                                                                                                                                                                                                                                                                                                                                                                                                          (HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEND-) MENDEL BIOTECHNOLOGY (REUB/) REUBER L.
                                                                                                                                                                                                                                                                                                                                                 2001-335979/35.
DB; AAE01933.
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) RIECHMANN J L.
) JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     YU G.
PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                         HEARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                          Creelman
Heard J;
                                                                                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                                                                                                                                                                                                                                                                                                                           Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                           Z,
                                                                                                                                                                                                                                                                                                                                                                                                           Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                          Jiang
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RESULT 4
ABK65362
ABK6
ACC ABC6
ACC ABC
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                      encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a that its polynucleotide is used for producing a plant having a recombinant polynucleotide is used for producing a plant having a that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-2000; 2000US-227439P.
16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agriculture; metal microbial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEND-)
(PILG/)
(CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK65362 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An isolated or recombinant polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ADAM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PINE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RIEC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KEDD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JIAN/
                                                                                                                                                                                                                                                                                                                                                                                        invention relates to 1 of 232 isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-292022/33.
)B; AAU93176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEARD J.
JIANG C.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADAM L.
RATCLIFF O.
REUBER J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M, Creelman
Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREELMAN R. DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIECHMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAACACCCATCTGAGTAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAACACTAATCTTCTAAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 877-878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene; transcription factor; transgenic;
e; metabolic chemical; environmental stress; drought;
disease resistance; herbicide resistance; seed yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding a transcription factor #214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R, Dubell AJ, Heard C
Reuber JL, Riechmann
                                                                                                                                                                                                                                                                                                                                                                                                                                           941pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used
                                                                                                                                                                                                                                                                                                                                                                                     or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keddie J;
Pineda O;
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RESULT 5
ABN98500/c
ID ABN985
XX ABN985
XX ASAbid
XX Arabid
XX Ara
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Best Local (
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(GORL/)
(ANYY/)
(HAMI/)
(PRIC/)
(RAIN/)
(YUYY/)
                                                                                                                                                                                                                                                             26-JAN-2001; 2001US-0770445.
                                                                                                                                                                                                                                                                                                                     21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                 US2002023281-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; disease; crop; thale cress; tolerance factor; insect; pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana expressed polynucleotide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN98500 standard; DNA; 982
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                                                                                                                                                                                                    27-JAN-2000; 2000US-178472P
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PRICE J L.
RAINES T M.
YU Y.
                                                                                                                                           GORLACH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                    AN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT
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Pred. No. 6.5e-37;
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(MATH/

MATHEW A V. RAMEAKA J G

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                                                                                                                                                                                                                                                                                                                          The invention relates to an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions CC to a sequence selected from any one of 99 sequences (ABN98231-ABN99231), CC given in the specification or its fragment. A polypeptide (II) encoded by CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a CC genetically modified cell (IV) comprising an exogenous nucleic acid, is CC useful in identifying homologous or related genes, in producing CC compositions that modulate the expression or function of its encoded CC protein, mapping functional regions of the protein and in studying a ssociated physiological pathways. (I) is also useful for the genetic CC manipulation of cells, particularly plant cells. (I) is also useful in CC screening assays of various plant strains to determine the strains that CC are best capable of withstanding a particular disease or environmental CC strees. (II) and (III) are useful for screening of biologically active CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical CC pathways. The screened agents are useful in improved methods of treating CC programs to identify agents that mimic or enhance the action of tolerance CC factors. Such agents are useful in improved methods of treating crops to CC enhance their tolerance to environmental stress. (I) is also useful for identifying other mediators that may induce constrained to the production of a biosynthetic product in a CC particular plant, for identifying other mediators that may induce tolerance to environmental stress, for identifying factors involved in biosynthetic pathways of nutritional, commercial or medicinal value and constrained or medicinal value.
                                                                            Matches
                                                                                            Query Match
Best Local 9
                                                                                                                                                                                       for identifying productions of nutritional, commercial or medicinal value. (IV) is useful in the study of genetic function and regulation, for alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene products. Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from USP at segdata.uspto.gov/sequence.html?DocID=999909770445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its
                                                                                                                                                        Sequence 982 BP; 303 A; 215 C; 140 G; 322 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded protein, and mapping functional regions of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-400781/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garcia
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(DAVI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GARC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WOES/
                                                           Local L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; SEQ ID NO 268; 49pp + Sequence Listing; English
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DAVIS K R.
ALLEN K.
HOFFMAN N.
                                                                                              Similarity
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GARCIA C A.
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WOESSNER J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRICKER M.
                                       TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA 78
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, Page A, M
Kricker M,
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                                                                                              22.5%;
74.5%;
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                                                                                              Score 186; DB 24;
Pred. No. 5.3e-36;
                                                                            Mismatches
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Hoffman N;
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17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription factor; trait modification; seed characteristic; structural characteristic; developmental characteristic; gene agricultural biotechnology; ss.
                                                           valetic acids encoding plant transcription factor polypeptides, useful for altering the developmental and structural characteristics of plants. e.g. corn. potato and cotton plants.
                                                                                                                                                                             WPI; 2001-335979/35.
                                                                                                                                                                                                                                                        Reuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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                                                                                                                                                      P-PSDB; AAE01916
                                                                                                                                                                                                                           Pineda
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                                                                                                                                                                                                                           Ó L
                                                                                                                                                                                                                                                                                                                           YU G.
PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                       RIECHMANN J L.
JIANG C.
                                                                                                                                                                                                                                                                                                      HEARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MENDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREELMAN R.
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                                                                                                                                                                                                                           Heard
                                                                                                                                                                                                                                                     Creelman
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; 2000US-0197899.
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Claim 4; Page 69-70; 133pp; English plants, e.g. corn, potato and

cotton plants

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wax content. They may also be used to alter seed characteristics such as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is Arabidopsis thaliana transcription factor G663 CDNA. The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify phrenyl lipid content, to modify fatty acid and modify seeds, to modify phrenyl lipid content, to modify fatty acid and modify
22-AUG-2000;
16-NOV-2000;
16-APR-2001;
                                                                                                                                                                                                plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1033 BP;
                                                                  22-AUG-2001;
                                                                                                   28-FEB-2002
                                                                                                                                    WO200215675-A1
                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                  Arabidopsis cDNA encoding a transcription factor #7.
                                                                                                                                                                                                                                                                                                                       02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                        ABK65155;
                                                                                                                                                                                                                                                                                                                                                                                       ABK65155 standard; cDNA; 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362
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Similarity 74.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTGGTCCTTGATTGCTGGTCGATTGCCTGGTCGGACCGCTAATGATGTCAAAAATTAC 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGATGCAGAAGAGTTGTAGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
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; 2000US-227439P.
; 2000US-0713994.
; 2001US-0837944.
                                                                  2001WO-US26189.
                                                                                                                                                                                                                                                                                                                       (first entry)
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Pred. No. 5.4e-36;
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GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC CĠĀTĠCAĠĀĀĀGĀĠŤŤĠŤĀĠĀĊŤĀĀĠĀŤĠĠŦŤĠĀĀCTĀŤTŤGĀĀĠĊĊĀĀGTĀŤĊĀĀĠĀĠĀ AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA

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                                                                                                                                                                                                                                                                                                                           composition in the sequence from a database comprising a plurality of known plant composition of the sequence sequence information selected from one of composition of the sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a composition of the sequence of the selecting a polynucleotide that composition of the sequence of the selecting a polynucleotide that composition of the selecting the selecting the selecting for a modified caid, inserting the composition of the selecting for a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified composition of agriculturally useful proteins or metabolic chemicals, composition of agriculturally useful proteins or met
                                                                                                                                                                                         Matches
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with a plant trait as compared to a wild plant. Also incluare a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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(PILG/)
(CREE/)
(DUBE/)
                                                                                                                                                                                                                                                                                                                        specification). The presenceding an A. thaliana
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(ADAM/)
(RATC/)
(REUB/)
(RIEC/)
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                                                                                            122
                                                                                                                                                                                         234;
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                                                                                                                                           19
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JIANG C.
KEDDIE J.
ADAM L.
RATCLIFF O.
REUBER J L.
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Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YU G.
PINEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREELMAN R.
DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIECHMANN J L.
1033
                                                                                            TCGTCCAAAGGGTTGAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGCTA
                                                                                                                                           TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                    BP; 334 A; 161 C; 226 G; 312 T; 0 other;
                                                                                                                                                                                                             22.5%;
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                                                                                                                                                                                         0;
                                                                                                                                                                                         Score 186; DB 24;
Pred. No. 5.4e-36;
0; Mismatches 80
                                                                                                                                                                                                                                        DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang C,
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                                                                                                                                                                                                                                        Length 1033;
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          This invention relates to the nucleotide and protein sequences of novel Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 or PAP2. The genes for both PAP1 and PAP2 have been mapped to chromosome 1. PAP1 and PAP2 have been mapped to chromosome 1. PAP1 and PAP2 are MYB-like transcription factors that regulate the production of anthocyanin pigment. The nucleotide sequence of the invention is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The nucleotide sequence is also useful for screening for plant cell (e.g., A. thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour
                                                                                                                                                                            Claim
                                                                                                                                                                                                 New isolated PAP1 or PAP2 gene, useful for increasing pigmentation in plants, as reporter genes for analysing expression pattern of promotes of interest, and to increase flux through phenylpropanoid pathway
                                                                                                                                                                                                                                                                                                         Borevitz J,
                                                                                                                                                                                                                                                                                                                                                                               23-JUN-2000; 2000US-0603244.
05-JUL-2000; 2000US-0610185.
                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2001; 2001WO-US19734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200200902-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic; plant; phenylpropanoid; stress; light stress; water stress; pH stress; temperature stress; heavy metal stress; pathogen attack; infection; wounding; nutrient deficiency; herbivory; plant colouration; stress sensitisation: gene, so, ohrowson, '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK14222 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A. thaliana Production of anthocyanin pigment 2 (PAP2) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                    (SALK )
                                                                                                                                                                                                                                                              2002-164443/21.
DB; AAU75735.
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                                                                                                                                                                                                                                                                                                                                    SALK INST BIOLOGICAL STUDIES ROBERTS NOBLE FOUND INC SAMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTGGTCCTTGATTGCTGGTCGATTGCCTGGTCGGACCGCTAATGATGTCAAAAATTAC 421
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                                                                                                                                                                                                                                                                                                         Xia Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product= "PAP2
                                                                                                                                                                      29pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                   alkaloid pathway gene; taxadiene synthase; biological pathway; freezing; abiotic stress; cold; drought; heat; nutrient deficiency; biotic stress; infection; developmental pathway; flowering; root development; TDS; LS; transgenic; transgenic plant; gene; ds
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                                                                                                                       WO200274917-A2
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription factor; metabolite pathway; terpenoid; limonene synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana G663 transcription factor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD47497 standard;
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/product= "Arabidopsis thaliana G663
/product= "Arabidopsis thaliana G663
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Pred. No. 5.4e-36;
0; Mismatches 80;
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15-MAR-2002; 2002WO-US07999.

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flowering, root development, a response pathway to environmental cues such as light intensity and light quality, circadian rhythm. Sequences of the invention are used to generate transgenic plants. The present sequence is Arabidopsis thaliana G663 transcription factor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining whether one of several test transcription factor (TF) polynucleotides encodes pathway TF by determining expression from pathway gene promoter linked to reporter gene in a cell in presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1033 BP; 334 A; 161 C; 226 G; 312 T; 0 other;
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                                                                                                                                                                                                                                                            GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATTAAGCTCTTAGGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                          TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT
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                                                                                       TGGAACACCCATCT
                                                                                                                       TGGAACACTAATCT 332
                                                                                                                                                                                             AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAAACTAT 318
                                                                                                                                                                                                                               GGAAGACTTAGCAATGATGAAGTTGATCTTCTTCTTCGCCTTCATAAGCTTCTAGGAAAT
                                                                                                                                                                                                                                                                                                    CGATGCAGAAAGAGTTGTAGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
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74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         relates to a high-throughput method for identifying hencodes a transcription factor for controlling the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 186; DB 25;
Pred. No. 5.4e-36;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a plant stress tolerance-related myloblastosis (MYB) transcription factor. The specification describes AtMYB60, AtMYB764, AtMYB75 and AtMYB90. MYB polypeptides are useful for enhancing a plant's tolerance or sensitivity to stress e.g. salt, drought, cold and heat tolerance. It is also useful for producing a transgenic plant with enhanced stress tolerance or stress sensitivity. MYB polypeptides are also useful for increasing the production of products of the phenylpropanoid biosynthesis pathway, e.g. stilbenes, flavonoids, lignins, salicylic acid, anthocyanins, and phenolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules encoding plant stress tolerance-related myloblastosis transcription factors for increasing stress resia crop in a field -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1043 BP; 334 A; 166 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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23-OCT-2000; 2000US-0693855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stress tolerance; myloblastosis transcription factor; heat tolerance; MYB transcription factor; AtMYB60; AtMYB764; AtMYB75; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of MYB transcription factor AtMYB90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Fig 4; 92pp;
                                                                                                                                                                                                                                                                   19 TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                    AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA
                                                 GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC
                                                                                                                                                            TGTATTGATAAGTATGGAGAAAGGCAAATGGCATCAAGTTCCTTTGAGAGCTGGGCTAAAT
                                                                                                                                                                                              TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCCATAAGAGCTGGTCTGAAT
                                                                                                                                                                                                                                   TCGTCCAAAGGGTTGAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGCTA
                     GGAAGACTTAGCAATGATGAAGTTGATCTTCTTCTTCGCCTTCATAAGCTTCTAGGAAAT
                                                                                         CGATGCAGAAAGAGTTGT
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                                                                                                                                                                                                                                                                                                                     22.5%;
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                                                                                          AGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                     Score 186; DB 22;
Pred. No. 5.4e-36;
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                       231 G;
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resistance

of.

for

312 T; 0 other;

80;

0,

Gaps

78

138 181

361

301 198 241

Length 1043; Indels

AAF85191 standard; cDNA; 1043 BP

78 147

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RESULT 11
AAD05767
ID AAD05
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The present cDNA sequence is homologue G2422 of Arabidopsis thaliana transcription factor G663. The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify the present of seeds as shalf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination
                                                                                                                                                                                Nucleic acids encoding plant transcription factor polypeptides, to for altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription factor; trait modification; seed characteristic; structural characteristic; developmental characteristic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001
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                                                                                                                                                                                                                                                                                         Reuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-2000; 2000WO-US31457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200135727-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD05767 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                        /NAIL)
                                                                                                                                                                                                                                                                                                                                                                                 (PILG/
                                                                                                                                                                                                                                                                                                                                                                                              (CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                         (REUB/
                                                                                                                                                                                                                                                   2001-335979/35
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                                                                                                                                                         4; Page 113; 133pp;
                                                                                                                                                                                                                                                                          0,5
                                                                                                                                                                                                                                                                                                                ) RIECHMANN J L.
) JIANG C.
) YU G.
) PINEDA O.
) HEARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                        MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                       AAE01932.
                                                                                                                                                                                                                                                                                                                                                                               PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                             CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                          REUBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAACACCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAACTAT
                                                                                                                                                                                                                                                                            Creelman
Heard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0166228
2000US-0197899
2000US-0227439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biotechnology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product= "Transcription factor homologue G2422"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
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R
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                                                                                                                                                                                                                                                                                        Pilgrim
                                                                                                                                                         English.
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                                                                                                                                                                                                                                                                                         Riechmann
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RESULT 12
ABK65363
ID ABK65
XX ABK65
XX ABK65
XX ABA65
XX Plant
XX
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Best Local S
Matches 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits.
                                                                                                                                                                                                                                                                                                                  22-AUG-2000; 2000US-227439P
16-NOV-2000; 2000US-0713994
16-APR-2001; 2001US-0837944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                        (DUBE/)
                                                                                                                                                                                                            (PILG/)
                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200215675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis cDNA encoding a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK65363 standard; cDNA; 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 741 BP; 237 A; 122 C; 174 G; 208 T; 0 other;
                        (RATC/)
                                                                             (KEDD/)
(ADAM/)
                                                                                                                               (JIAN/)
                                                                                                                                                                                                                                                                   (MEND-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
RATCLIFF O.
REUBER J L.
RIECHMANN J L.
                                                                                             CREELMAN R.
DUBELL A J.
HEARD J.
JIANG C.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                               CREELMAN
                                                                                                                                                                                                                                                                   MENDEL BIOTECHNOLOGY
                                                                          ADAM L.
                                                                                                                                                                                                                                          PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTATTGCTGGTAGACTTCCCCGGAAGGAACACTATAGGAACACTATTGGAACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAATAGATGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATTTGAGTAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATCTTCTAAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGATCGCTGGTAGATTGCCTGGTCGGACTGCTAATGATGTCAAGAATTACTGGAACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAACAAGATGAAGTGGATCTCATTTTGAGGCCTTCATAAGCTCTTAGGCAACAGATGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGTATGGAGAAGGCAAATGGCATCGAGTTCCTTTAAGAACTGGTCTCAATCGGTGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTTGAGAAAAGGTACATGGACTACTGAAGAAGATATTCTCTTGAGGCAATGCATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTCCGATGAAGTTGATCTTGTTCTTCGCCTTCATAAACTTCTAGGAAATAGGTGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGAGTTGTAGACTTAGATGGTTGAATTATTTGAAGCCAAGTATTAAGAGAGGAAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342
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                                                                                                                                                                                                                                                                   INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 185.4; DB 2
Pred. No. 6.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC encoding an Arabidopsis thaliana transcription factor, their variants, CC complements, fragments, or related polynucleotide with 31% to 95% CC sequence identity, where the plant polynucleotide with 31% to 95% CC sequence identity, where the plant polynucleotide with 31% to 95% CC sequence identity, where the plant polynucleotide with 31% to 95% CC sequence identity, where the plant, or the plant exhibits an altered CC phenotype as compared to a wild-type or reference plant, or the plant CC exhibits ectopic expression or altered expression of one or more genes CC associated with a plant trait as compared to a wild plant. Also included associated with a plant trait as compared to a wild plant. Also included CC are a transgenic plant comprising the polynucleotides, a computer CC readable medium having stored sequence information, and identifying a CC homologue sequence from a database comprising a plurality of known plant CC sequences comprising sequence information selected from one of CC 464 fully defined sequences given in the specification. The isolated or CC encodes a polynucleotide is used for producing a plant having a CC encodes a polynucleotide or an antisense nucleic acid, inserting the CC polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress CC plant, and selecting for a modified trait (e.g. increased chemicals, post tolerance, herbride resistance, seed and fruit yield, growth CC pest tolerance, herbride resistance, seed and fruit yield, growth CC trate, leaf and flower sensescence and many other traits listed in the CC encoding an A. thaliana transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-292022/33.
P-PSDB; AAU93177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 741 BP; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (YUGG/) YU G. (PINE/) PINEDA O.
319
                                                                                                                                                             199
                                                                                                                                                                                                                                                                                       148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Page 879-880; 941pp; English
                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M, Creelman
Ratcliff O,
CATTTGAGTAAGAAG
                                                                                                                 CTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAAACTATTGGAACACT
                                                                                                                                                               TGCTCCGATGAAGTTGATCTTGTTCTTCGCCTTCATAAACTTCTAGGAAATAGGTGGTCC
                                                                                                                                                                                                    GAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCA
                                                                                                                                                                                                                                                                                   AAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGAGGTGACTTT
                                                                                                                                                                                                                                                                                                                                                                        AAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAATAGATGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGAT
                                      AATCTTCTAAGGAAG 342
                                                                              TTGATCGCTGGTAGATTGCCTGGTCGGACTGCTAATGATGTCAAGAATTACTGGAACACT
                                                                                                                                                                                                                                              AAGAGTTGTAGACTTAGATGGTTGAATTATTTGAAGCCAAGTATTAAGAGAGAAAACTC
                                                                                                                                                                                                                                                                                                                               AAGTATGGAGAAGGCAAATGGCATCGAGTTCCTTTAAGAACTGGTCTCAATCGGTGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                              GGGTTGAGAAAAGGTACATGGACTACTGAAGAAGATATTCTCTTGAGGCAATGCATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 122 C; 174 G; 208 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R, Dubell AJ, Heard J, i
Reuber JL, Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 185.4; DB 2
Pred. No. 6.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jiang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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Pineda O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        741;
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RESULT 13

Query Match Best Local Similarity

21.8%;

Score 180.2; DB 2 Pred. No. 1.4e-34;

DB 24; Length 956;

Sequence

956

BP;

310 A; 162 C; 202 G; 282 T; 0 other;

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ABK14221
                                             CC Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 CC Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 CC Arabidopsis thaliana production of anthocyanin pigment paye been mapped to chromosome C1. PAP1 and PAP2 are MYB-like transcription factors that regulate the CC invention is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The CC useful for detecting promoter activity within a plant cell sequence is also useful for screening for plant cell (e.g., CA, thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour cexpression. The nucleotide sequence is also useful for enhancing CC expression of phenylpropanoid product in a plant. A transgenic CC plant is useful for detecting a stress condition such as light CC stress, water stress, pH stress, temperature stress, heavy metal constress, water stress, pH stress, temperature stress, heavy metal constress, water stress, pH stress, temperature stress, heavy metal constress, pathogen attack or infection, wounding, nutrient deficiency, CC herbivory, or abnormal hormone levels in a plant. PAP1 or PAP2 constitution in ornamental plants for commercial sales, and for colouration in ornamental plants for commercial sales, and for colouration of plants to respond more quickly to a stress condition in ways that are physiologically significant, as well as in ways of ornamental CC sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAP1; production of anthocyanin pigment; MYB-like transcription factor; transgenic; plant; phenylpropanold; stress; light stress; water stress; bH stress; temperature stress; heavy metal stress; pathogen attack; infection; wounding; nutrient deficiency; herbivory; plant colouration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated PAP1 or PAP2 gene, useful for increasing pigmentation in plants, as reporter genes for analysing expression pattern of promoter of interest, and to increase flux through phenylpropanoid pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK14221 standard; cDNA; 956 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 26; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borevitz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-2000; 2000US-0603244.
05-JUL-2000; 2000US-0610185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-2001; 2001WO-US19734.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. thaliana Production of anthocyanin pigment 1 (PAP1) cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SALK ) SALK INST BIOLOGICAL STUDIES (ROBE-) ROBERTS NOBLE FOUND INC SAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sensitisation; gene; ss; chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xia Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                        invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "PAP1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                       cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-2000; 2000US-227866P.
26-JAN-2001; 2001US-264647P.
22-JUN-2001; 2001US-300111P.
                                                                                                                                                                                                                          Identifying a stress and producing plants
                                                                                                                                                                                                                                                                                                                                                                                                      (SCRI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana; plant; gene; stress; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ14829 standard; DNA; 747
                                                                                                                                                                                                                                                                                                                                                    Harper JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-2001; 2001WO-US26685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2002
                                                                                           invention relates to identifying a stress
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SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAACACTAATCTTCTAAGGAAGTTAAATACTACTAAAATTGTTCCTCGCGAAAAGATT
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                                                                                                                                               SEQ ID NO 2634; 577pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                    Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                          condition to which a plant cell has been exposed with increased tolerance to these abiotic stress
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                                                                                                                                                                                                                                                                                                                                                    Wang X,
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Best Local S
Matches 233
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Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; microbial disease resistance; see fruit yield; growth rate; leaf senescence; flower senes
                                                                                                                                                      22-AUG-2000; 2000US-227439P
16-NOV-2000; 2000US-0713994
16-APR-2001; 2001US-0837944
                        (MEND-)
(PILG/)
(CREE/)
(DUBE/)
                                                                                                                                                                                                                                                           22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                                                                              28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                 WO200215675-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis cDNA encoding a transcription factor #193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK65341;
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233; Conserv
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CREELMAN R.
DUBELL A J.
HEARD J.
                                                                                                     MENDEL
                                                                                PILGRIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAACACTAATCTTCTAAGGAA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGTGCAGGAAAAGTTGTAGATTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGTCCAAAGGGCTGCGAAAAGGTGCTTGGACTACTGAAGAAGATAGTCTCTTGAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGAAGAAGATTTTCTTCTAAGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGTGGTCTTTAATTGCTGGAAGATTACCTGGTCGGACCGCAAATGACGTCAAGAATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAACTAT
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ilarity 72.1%;
Conservative
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Pred. No. 2.6e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24;
2.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    senescence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated with a plant trait as compared to a wild plant. Also included CC are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a composition of the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant; and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rate, lear and respect segments segment segments encoding an A. thaliana transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes exhibits ectopic expression or altered expression of one or more genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pest tolerance, environmental stress response (e.g. drought), microbia disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pilgrim M, Creelman
Adam L, Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KEDD/)
(ADAM/)
(RATC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 925 BP; 290 A; 160 C; 200 G; 275 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 792-794; 941pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-292022/33.
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RATCLIFF O.

REUBER J L.

RIECHMANN J L.

YU G.

PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JIANG C.
KEDDIE J.
                                                                                                                                                                                                    AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCCACATATCAAGAGA 198
                                                                                                                                                                                                                                                                                                                                                             TCTTCATTGGGAGAGAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA 78
                                        AGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAACTAT 318
                                                                                                                          GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC 258
                                                                                                                                                                   CGGTGCAGGAAAAGTTGTAGATTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
                                                                                                                                                                                                                                                                         TGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT 138
                                                                                                                                                                                                                                                                                                                                     TCGTCCAAAGGGCTGCGAAAAGGTGCTTGGACTACTGAAGAAGATAGTCTCTTGAGACAG 127
                                                                                 GGAAAACTTAGCTCTGATGAAGTCGATCTTCTTCTTCGCCTTCATAGGCTTCTAGGGAAT
                                                                                                                                                                                                                                                   TGCATTAATAAGTATGGAGAAGGCAAATGGCACCAAGTTCCTGTAAGAGCTGGGCTAAAC 187
  AGGTGGTCTTTAATTGCTGGAAGATTACCTGGTCGGACCGCAAATGACGTCAAGAATTAC 367
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    21.7%;
72.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 179; DB 24; Length Pred. No. 2.7e-34; O; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     90; Indels
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L, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Keddie J;
Pineda O;
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                                                                                 307
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      Qy
      319 TGGAACACTAATCTTCTAAGGAA 341

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      Db
      368 TGGAACACTCATCTGAGTAAGAA 390
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Search completed: January 30, 2004, 07:19:18
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfIles1.seq:*
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Gapop 10.0 , Gapext 1.0
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
       4 US-09-610-185C-3
4 US-09-610-185C-1
2 US-09-608-792-628-1
3 US-09-008-979A-2
3 US-09-460-618-2
4 US-09-402-929-1
4 US-09-402-929-1
4 US-09-402-929-1
5 US-09-402-929-1
6 US-09-402-929-1
7 US-09-402-929-1
8 US-09-10-2518-6
8 US-09-10-2518-6
8 US-09-110-2518-6
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8 US-09-110-2518-6
8 US-09-110-2528-1
9 US-09-167-322-10
9 US-08-306-6118-4
9 US-08-306-6118-4
9 US-08-485-139-1
9 US-08-485-139-1
9 US-08-485-139-5
9 US-08-750-357-1
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319 TGG	259 AG    362 AG	199 GG    302 GG	139 AG       242 CG	79 TG    182 TG	19 TC	Match ocal Simi s 234;	28 44.2 5.4 29 44.6 5.2 30 42.6 5.2 31 42.6 5.2 31 42.6 5.2 32 42.6 5.2 33 42.6 5.2 34 42.6 5.2 35 42.6 5.2 36 42.6 5.2 37 42.6 5.2 38 42.4 5.1 39 42.6 5.2 37 42.6 5.2 38 42.4 5.1 39 42.4 5.1 39 42.4 5.1 39 42.4 5.1 39 42.4 5.1 39 42.4 5.1 39 42.4 5.1 39 6 4.8 41 5.0 41 41.6 5.0 42 41 5.0 43 41 5.0 43 41 5.0 44 39.6 4.8 45 39.6 4.8 45 39.6 4.8 45 39.6 4.8 45 39.6 4.8 45 39.6 4.8 45 39.6 4.8 45 39.6 4.8 47 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.
TGGAACACTAATCT	AGATGGTCACTTATTC	TGACTTTG    AAGACTTA	ATGTCGGA         ATGCAGAA	TATTGATA         TATTGATA	TTCATTGG    GTCCAAAG	22. ilarity 74. Conservative	14.2 5.4 1891 3 US-08 12.6 5.2 835 4 US-09 12.6 5.2 1714 3 US-09 12.6 5.2 5361 3 US-08 12.6 5.2 5361 2 US-09 12.6 5.2 15213 4 US-09 12.6 5.1 825 4 US-09 12.6 5.0 19124 2 US-09 13.6 5.0 19124 2 US-09 14.1 5.0 319608 4 US-09 14.1 5.0 319608 4 US-09 14.1 5.0 319608 4 US-09 15.0 319608 4 US-09 17.1 Sapplication US/09610185C 185C-3 1 US-08 185C-3
ATCT 332	TTATTGCTG	AACAAGAT       GCAATGAT	AAAGTTGT         AGAGTTGT	AGTATGGT        AGTATGGA	GAGTGAGA           GGTTGAGG	22.5%; 74.5%; ative	1891 3 U 835 4 U 1714 3 U 1714 3 U 5361 3 U 6215 3 U 6213 4 U 5889 4 U 19124 2 U 192478 4 U 2478 4 U 2478 4 U 2732 1 U 2733 1 U 2734 1 U 2735 1 U 2736 1 U 2737
	GGTAGACT          GGTCGATT	GAAGTGGA         GAAGTTGA	AGATTGAG	GAAGGAAA       GAAGGCAA	AAAGGTTC        AAAGGTGC	Score Pred. : 0; Mis	28 44.2 5.4 1891 3 US-08-97 29 42.6 5.2 835 4 US-08-95 30 42.6 5.2 1714 4 US-09-53 31 42.6 5.2 1714 4 US-09-53 32 42.6 5.2 1714 3 US-08-96 33 42.6 5.2 5340 4 US-09-53 34 42.6 5.2 5361 3 US-08-97 35 42.6 5.2 6152 3 US-08-97 36 42.4 5.1 5889 4 US-09-96 37 42.6 5.2 15213 4 US-09-96 38 42.4 5.1 5889 4 US-09-40 38 42.4 5.1 5889 4 US-09-40 41 41.6 5.0 19124 2 US-08-97 42 41 5.0 319608 4 US-09-53 C 42 41 41.6 5.0 19124 2 US-08-47 45 39.6 4.8 2732 1 US-08-47 45 39.6 5.7 19124 2 US-09-610 Sequence 3, Application US/09610185C Patent No. 6573432 GENERAL INFORMATION: APPLICANT: Borevitz, Justin APPLICANT: Dixon, Richard A. APPLICANT: Dixon, Richard A. APPLICANT: Lamb, Christopher J. TITLE OF INVENTION: PRODUCTION FILE REFERENCE: SALKINS.003C1 CURRENT PILING DATE: 2000-07-05 PRIOR APPLICATION NUMBER: US/09/610, PRIOR PILING DATE: 2000-06-23 NUMBER: FastSEQ for Windows Version SEQ ID NO 3 LEGGTH: 1033 TYPE: DNA ORGANISM: Arabidopsis thaliana
	AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAAACTAT 	GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC 	agatgtcggaaaagttgtagattgaggtggctgaattatctaaggccacatatcaagaga 	TGTATTGATAAGTAIGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT 	TCTTCATIGGAGIGAAAAGGTICATGGACTGATGAAGAAGATTTTCTICTAAGAAAA 	re 186; DB d. No. 2.8e- Mismatches	3-462-3 1-083-93 1-083-93 1-083-3 1-122-21 1-122-21 1-122-21 1-122-21 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128-52 1-128
	GACAGCTAJ          GACCGCTAJ	GAGGCTTC:        TCGCCTTC:	TTATCTAA	TGTTCCCA	TGAAGAAG!          TGAAGAAG!	4; Le 39; 80;	PIGMENT
	ACGATGTGA           ATGATGTCA	ATAAGCTCT        ATAAGCTTC	GGCCACATA        AGCCAAGTA	TAAGAGCTG            TGAGAGCTG	ATTTTCTTC        ATAGTCTCT	1033; le	Sequence
	AAAACTAT         AAAATTAC	TAGGCAAC	TCAAGAGA           TCAAGAGA	GTCTGAAT	TAAGAAAA        TGAGGCTA	0; Gaps	600, 138, 20, 11, 12, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13
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RESULT 3
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; TYPE: DNA
; ORGANIEM: Arabidopsis Thaliana
US-09-610-185C-1
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US-09-610-185C-1
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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                                                                 GENERAL INFORMATION:
APPLICANT: Yang, Yinong
APPLICANT: Yang, Yinong
APPLICANT: Klessig, Daniel, F.
APPLICANT: NOVEL GENES ASSOCIATED WITH ENHANCED
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/610,185C
CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: US 09/603,244
PRIOR FILING DATE: 2000-06-23
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APPLICANT: Lamb, Christopher J.
TITLE OF INVENTION: REGULATION OF ANTHOCYANIN PIGMENT
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: SALKINS.003C1
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APPLICANT: Xia, Yiji
APPLICANT: Dixon, Richard /
APPLICANT: Lamb, Christoph
                               CORRESPONDENCE ADDRESS:
                                                      NUMBER OF SEQUENCES:
ADDRESSEE:
STREET: 1
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Local Similarity 68.0%;
les 251; Conservative
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3: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
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; LOCATION: 148...981
; OTHER INFORMATION:
US-08-722-626B-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Pat Hagan
REGISTRATION UNMBER: 27,643
REFERENCE/DOCKET NUMBER: 97-0
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 215 563-4044
TELEPAX: 215 563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 27-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 AATGGGGCTGAAAAAAAGGGCCATGGATTCCTGAAGAAGATCAGATTCTCATCTCTTTCAT
                  534 CAAGT 538
                                                                                                                                                                                                                                                                                                                                              144 TCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGAGGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                          84 TGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAATAGATG
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                                                      TAAGT 388
                                                                                                                             CACTAATCTTCTAAGGAAGTTAAATACTACTAAAATTGTTCCTCGCGAAAAGATTAACAA 383
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                                                                                          CACCCACTTGAAGAAGCTCAAAGATTATAAGCCTCCTCAGAACTCCAAAAGACACTC
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                                                                                                                                                                                                                      Sequence 2, Application US/09460618 Patent No. 6235482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.3%;
Best Local Similarity 74.0%;
                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (713) 789-26
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Conner
                                                                        APPLICANT: Conner, Timothy W.

TITLE OF INVENTION: Strawberry Promoters and Genes

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carmen Rodriguez, Paralegal, Arnold, White & Durkee

STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:058 (38-21(10613)A)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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COMPUTER READABLE FORM:
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ZIP: 77210-4433
                                                     STATE:
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               COUNTRY: USA
ZIP: 77210-4433
                                                                      STREET: P.O. CITY: Houston
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                                                     Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 85.2; DB 3; Pred. No. 3.4e-13;
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                                                                                                                     Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09310235B Patent No. 6392030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 108;
                                                                                                                                                   Query Match
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                                                                                                                                                                                             TYPE: DNA
ORGANISM: fragaria x ananassa
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:058 (38-21(10613)A)
TELECOMMUNICATION INFORMATION:
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NAME: Kammerer, Patricia A.
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APPLICATION NUMBER:
                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                            182 GGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTC 241
                                                                                       122 TAAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 ATAAGCTCTTAGGCAACAGATGGTCA 267
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                                                                                                                    Score 85.2; DB 4;
Pred. No. 3.4e-13;
0; Mismatches 38
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Pred. No. 3.4e-13;
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                                                                                                                                                Length 469;
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                                                                                                                       Indels
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                  Matches 177;
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND TITLE OF INVENTION: USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/402,929
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                                                                                                                                     471
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                       268
                                                             531 ACAGAAGAGGACAGGATCATCTATGAAGCACATAAGCGGTTGGGAAATCGTTGGGCA
                                                                                                                                                                                                              414 AAATATGGGCCAAAAAGATGGTCTTTAATTGC---AAAACATTTAAAAGGAAGAATAGGC 470
                                                                                            208 GAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCA 267
                                                                                                                                                                                                                                                                                                                          28 GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGAT 87
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EDNESS: single
CTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTATTGGAACACT 327
                                                                                                                                     ÁAGCAGTGTÁGÁGAAAGATGGCATÁÁTCATCTGÁATCCTGAGGTAAAGAAATCTTCCTGG 530
                                                                                                                                                                         AAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGAGGGGACTTT 207
                                                                                                                                                                                                                                                    AAGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAATAGATGTCGG 147
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Suite 1800 Two Penn Center Plaza
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Hatton, Kimi
Reddy, E. P.
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Pred. No. 2e-12;
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                                                                                                             US-08-997-251-1
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                                                 Matches 160;
                                                            Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 2220 base pairs
                                                                                                                                                          FEATURE:
                                                                                                                                                                                         TISSUE TYPE: A
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: PLANT REGULATORY PROTEINS
                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                            NAME/KEY:
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STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Winner, Ellen P. REGISTRATION NUMBER: 28,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO AU96/00383
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                                                                                                                                                                                                                         ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 ACTATGCGAAGAAA 664
32 TGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTACTAAGAAAATGTATTGATAAGT 91
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                                                 0; Mismatches 136;
                                                               Score 78.4; DB 3;
Pred. No. 3.4e-11;
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US-09-402-929-1
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                                                                                                                Query Match
                                                                                                                                                                                                                                                   TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Temple
                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hatton, Kimi
APPLICANT: Reddy, E. P.
TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND
TITLE OF INVENTION: USES THEREOF
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Monaco, Daniel A.
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                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCACTTA
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                                                                                                                                                                                     nucleic acid
DEDNESS: single
                                                                                           Similarity
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GAATTGATAAAGGGTCCTTGGACTAAGGAAGAAGATCAGAGGGTTATTGAATTAGTTCAG
                                    GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGAT 87
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                                                                                           Score 77.2; DB 4;
Pred. No. 8.3e-11;
                                                                           Mismatches
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                                                                                                                          US-09-402-929-4
                                                                 Query Match
Best Local Similarity
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GENERAL INFORMATION:
                                                     Matches
                                                                                                                                                                                                                           TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                               NAME: Monaco, Daniel A. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SEIDEL, GOND STREET: Suite 1800 Two
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 CTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTATTGGAACACT
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28 GGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAGGAAAAATGTATTGAT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 AAGTATGGTGAAGGAAAATGGCATCTTGTTCCCCATAAGAGCTGGTCTGAATAGATGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19102
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                                                                                                                                                                                          6775 base pairs
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Toscani, And
Toscani, Kimi
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Reddy, E.
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Temple University - Of The Commonwealth System of Higher Education
                                                                                                                                           linear
                                                                   9.4%;
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Two Penn Center Plaza
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                                                                 Score 77.2; DB 4;
Pred. No. 1e-10;
                                                     Mismatches 138;
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                                                                                  Length 6775;
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                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,251
FILING DATE: 23-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: AU PN6470/95
FILING DATE: 09-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN3779/95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN3779/95
PRIOR APPLICATION UNDER: AU PN3779/95
PRICATION DATA:
APPLICATION NUMBER: AU PN3779/95
PRICATION DATA:
APPLICATION NUMBER: AU PN3779/95
PRICATION DATA:
APPLICATION NUMBER: AU PN3779/95
PRICATION DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GUBLER, FRANZ J.
APPLICANT: JACOBSEN, JOHN V.
TITLE OF INVENTION: PLANT REGULATORY PROTEINS III
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Boulevard
                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                        NAME: Winner, Ellen P.
REGISTRATION NUMBER: 28,547
REPERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 5370
CITY: Boulder
                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 GAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGATTGCTAAGTTACTTCCTGGAAGGACTGATAATTCTATCAAAAATCATTGGAATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGAAGAAGAAGACAGGATCATATATGAAGCACACAAGCGCCTGGGAAACCGTTGGGCC
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                                                                                                                                                       2352 base pairs
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LOCATION:
US-08-997-251-3
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US-09-008-979A-6
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Query Match
Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09008979A Patent No. 6080914
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                       TELEFAX: (713) 789-26 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:058 (38-21(10613)A)
                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IF PC COMPATIBLE
COMPUTER: FLOPPY
COMPUTER: PC-DDS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (713) 787-1438 TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: Conner, Timothy W. ITLE OF INVENTION: Strawberr
                                                                                                                STRANDEDNESS:
                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 AAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCACTTA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 TGAAGAAGGGGCCATGGACGTCGGCGGAGGACGCCATCCTGGTGGACTACGTGAAGAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 ATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAATAGATGTCGGAAAA 151
                                                                                                                             nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGGCGAGGGGAACTGGAACGCGGTGCAGAAGAACACCGGGCTGTTCCGGTGCGGCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Carmen Rodriguez, Paralegal, Arnold, White & Durkee P.O. Box 4433
   8.7%;
nilarity 61.3%;
Conservative
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Pred. No. 2.4e-10;
     Score 71.4; DB 3;
Pred. No. 1.6e-09;
0; Mismatches 81
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                                           Length 785;
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RESULT 13
US-09-460-618-6
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Best Local Similarity
Matches 133; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 785 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kammerer, Patricia A. REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                          TOPOLOGY:
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ilarity 61.3%;
Conservative
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                                                                                                                                                                                               Score 71.4; DB 3;
Pred. No. 1.6e-09;
0; Mismatches 81;
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; SEQ ID NO 6
TENCTH: 785
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Patent No. 5670367
GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Paterer*
EQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09310235B Patent No. 6392030
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Best Local Similarity
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TYPE: DNA
ORGANISM: fragaria x ananassa
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OTHER INFORMATION: N = A, T, C or G
             ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                               CITY: Alexandria
                                                                                                                                                                                    STREET:
                                                                                                                             COUNTRY:
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1800 Diagonal Road,
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Pred. No. 1.6e-09;
                                                                                                                                                                                    Suite 500
                   Version
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Search completed: January 30, 2004, 08:33:09 Job time: 64 secs
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US-08-232-463-14
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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8.4%; Score 69.6; DB 1; Length 7218;
Best Local Similarity 7.0%; Pred. No. 1e-08;
Matches 30; Conservative 233; Mismatches 167; Indels 0.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                          185.4
179
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1: /cgn2_6/ptodata/1/pubpna/US07
2: /cgn2_6/ptodata/1/pubpna/PCT
3: /cgn2_6/ptodata/1/pubpna/US06
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/cgn2_6/ptodata/1/pubpna/US09B PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10B_NEW_PUB.seq:*
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IS US-10-295-403-43

II US-09-934-455-13

II US-09-934-455-481

IO US-09-938-842A-2634

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Sequence 479, App
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Sequence 13, Appl
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Sequence 437, App
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Sequence 5, Appli
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RESULT 1 US-10-033-190-1

## ALIGNMENTS

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Sequence 1, Application US/10033190
Publication No. US20020133848A1
GENERAL INFORMATION:
APPLICANY: Exelixis Plant Sciences, Inc.
TITLE OF INVENTION: IDENTIFICATION AND CHARA
TITLE OF INVENTION: TOMATO
FILE REFERENCE: EPO1-002C
CURRENT APPLICATION NUMBER: US/10/033,190
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION USER: US/0/244,685
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
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; ORGANISM: Lycopersicon esculentum
US-10-033-190-1
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Best Local Similarity 100.
Matches 825; Conservative
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181 AGGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTT 240
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                                      ATAAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTA
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100.0%; Pred. No. 4e-179;
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APPLICANT: Exelixis Plant Sciences, Inc.
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF
TITLE OF INVENTION: TOMATO
FILE REFERENCE: EP01-002C
CURRENT APPLICATION NUMBER: US/10/033,190
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/244,685
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 1012
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; TYPE: DNA
; ORGANISM: Lycopersicon
US-10-033-190-4
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Best Local S
Matches 825
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Pred. No. 1.2e-131;
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                                        RESULT 3
US-09-934-455-479
Sequence 479, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
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Sequence 268, Application US/09770445
Patent No. US20020023281A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An. Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
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US-09-770-445-268/c
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; LOCATION: (1)..(630)
; OTHER INFORMATION: G2421
US-09-934-455-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR PPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 479
LENGTH: 762
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Best Local Similarity
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APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant
FILE REFERENCE: MSI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
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APPLICANT:
 APPLICANT:
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Pilgrim, Marsha
Ratcliffe, Oliver
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Jiang, Cai-Zhong
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Yu, Yang
Rameaka, Joshua
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US-10-295-403-43
Sequence 43, Application US/10295403
; Publication No. US20030101481A1
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Broun, Pierre Pineda, Omaira Reuber, Lynne Jiang, Cai-Zhong Keddie, James Zhang, James

APPLICANT:

APPLICANT: APPLICANT:

Riechmann, Jose Luis Adam, Luc

Jacqueline

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SEQ ID NO 268
LENGTH: 982
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Best Local Similarity
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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
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APPLICANT:
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APPLICANT:
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                      319 TGGAACACTAATCT 332
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                                                                                         AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAAACTAT 318
                                                                                                                                                      GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC 258
                                                                                                                                                                                                      CGATGCAGAAAGAGTTGTAGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
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TGGAACACCCATCT 598
                                                                                                                                   GGAAGACTTAGCAATGATGAAGTTGATCTTCTTCTTCGCCTTCATAAGCTTCTAGGAAAT
                                                                AGGTGGTCCTTGATTGCTGGTCGATTGCCTGGTCGGACCGCTAATGATGTCAAAAAATTAC
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Woessner, Jeffrey P.
Haas, William David
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Slader, Ted
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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74.5%;
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Pred. No. 1.2e-32;
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Fromm, Mike

Benito, Maria-Ines

Guo-Liang

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RESULT 6
US-09-934-455-13
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; LOCATION: (96)..(842)
; OTHER INFORMATION: G663
US-10-295-403-43
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FILE REFERENCE: MBI-0003
CURRENT APPLICATION NUMBER: US/10/295,403
CURRENT APPLICATION NUMBER: US/09/394,519
PRIOR APPLICATION NUMBER: US/09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/108,734
PRIOR APPLICATION NUMBER: 60/108,734
PRIOR APPLICATION NUMBER: 60/113,409
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-12-22
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LENGTH: 1016
TYPE: DNA
                                                                                                                                                                                                              Sequence 13, Application US/09934455 Publication No. US20030121070A1
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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SOFTWARE: PatentIn Ver. 2
  APPLICANT:
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                                                          APPLICANT:
                                    PPLICANT:
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                                                                                                                                                                                                                                                                                                                              TGGAACACCCATCT 418
                                                                                                                                                                                                                                                                                                                                                                    TGGAACACTAATCT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCTAACGATGTGAAAAACTAT 318
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                                                                        Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
Keddie, James
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Reuber, Lynne
Riechmann, Jo
                                      Pilgrim, Marsha
Ratcliffe, Oliver
                                                                                                                                                  Creelman, Robert
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  Jose Luis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 186; DB 15;
Pred. No. 1.2e-32;
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)..(862)
; OTHER INFORMATION: G663
US-09-934-455-13
                                                                                                                                                                                                                                                                                                             US-09-934-455-481; Sequence 481, Application US/09934455; Publication No. US20030121070A1
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APPLICANT: Pineda, Omaira
ITITLE OF INVENTION: Genes for Modifying Plant Tri
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Adam, Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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              APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
                                                                                                                 APPLICANT:
CURRENT APPLICATION NUMBER: US/09/934,455
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                                                                                                                                                                                          Creelman, Robert
Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
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                                                                      Riechmann, Jose Luis
Yu, Guo-Liang
                                                                                                               Reuber, Lynne
                                                                                                                                 Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
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Pred. No. 1.2e-32;
0; Mismatches 80,
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361

258

241

181 78

FILING DATE:

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2634
LENGTH: 747
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PRIOR FILLING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILLING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILLING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
SEQ ID NO 481
LENGTH: 741
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; NAME/KEY: CDS
; LOCATION: (1)..(741)
; OTHER INFORMATION: G2422
US-09-934-455-481
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Best Local Similarity
LENGTH: 747
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGAGTTGTAGACTTAGATGGTTGAATTATTTGAAGCCAAGTATTAAGAGAGGAAAACTC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGTATGGAGAAGGCAAATGGCATCGAGTTCCTTTAAGAACTGGTCTCAATCGGTGCCGA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2634
LENGTH: 747
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3 CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR PILING DATE: 2000-08-24 PRIOR PILING DATE: 2001-08-24 PRIOR PILING DATE: 2001-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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CGGTGCAGGAAAAGTTGTAGATTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGA
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                                                                                                                                         TGCATTAATAAGTATGGAGAAGGCAAATGGCACCAAGTTCCTGTAAGAGCTGGGCTAAAC 129
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 4.2e-31;
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Pred. No. 4.2e-31;
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SEQ ID NO 437
LENGTH: 925
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (59)...(697)
OTHER INFORMATION: G1329
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US-09-934-455-437
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Best Local Similarity
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APPLICANT:
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TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR PILING DATE: 2000-08-22
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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NUMBER OF SEQ ID NOS: 516
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PRIOR FILING DATE: 2001-04-17
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                                                                                                                                                                                                                                          19 TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA 78
                                                                                                                                                                                                                                                                                           233;
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                                 GGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAAC 258
                                                                                           AGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGA 198
                                                                                                                                            TGCATTAATAAGTATGGAGAAGGCAAATGGCACCAAGTTCCTGTAAGAGCTGGGCTAAAC
                                                                                                                                                                 TGTATTGATAAGTATGGTGAAAGGAAAATGGCATCTTGTTCCCATAAGAGCTGGTCTGAAT 138
                                                                                                                                                                                                                  TCGTCCAAAGGGCTGCGAAAAGGTGCTTGGACTACTGAAGAAGATAGTCTCTTGAGACAG 127
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GGAAAACTTAGCTCTGATGAAGTCGATCTTCTTCTTCGCCTTCATAGGCTTCTAGGGAAT
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Pilgrim, Marsha
Ratcliffe, Oliver
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Dubell, Arnold
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Riechmann, Jose Luis
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                        Score 179; DB 11;
Pred. No. 4.6e-31;
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US-09-443-704-5

Sequence 5, Application US/09443704
Patent No. US20020066120A1
GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca APPLICANT: Liu, Zhan-Bin APPLICANT: Odell, Joan

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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
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SEQ ID NO 2454
LENGTH: 390
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Best Local Similarity
Matches 227; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1). (390)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-024-Q1-B1-G6
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                                      340 AAGTTAAATACTACTAAAATTG 361
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                                                                                                                                                              216 GTGGAAATGATAATCAAACTCCATAAATTACTAGGCAACAGATGGTCGTTGATTGCACGA
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                                                                                                                                                                                                                                            156 CTAAGATGGCTGAACTATCTCCGTCCTAACATCAAGAGAGGAAATTTTGCGGAGGAAGAA
                                                                                                                                                                                                                                                                            160 TTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGAGGTGACTTTGAACAAGATGAA 219
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336 AAACTAAATGTAATAGAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                           36 GTTGCATGGACAGAAGAAGATCACTTGCTCAAGAAATGCATACAACAATATGGAGAA
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                                                                                                                                                                                                                                                                                                                            GGAAAGTGGCATCGTGTTCCTTTACTGGCTGGTTTAAACAGGTGCCCGGAAGAGTTGTAGG 155
                                                                                                         AGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTATTGGAACACTAATCTTCTAAGG
                                                                                                                                                                                                    GIGGAICTCATTTIGAGGCTICATAAGCTCTTAGGCAACAGAIGGTCACTTATTGCTGGI 279
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                                                                              AGGCTACCAGGAAGGACTGCCAATGATGTGAAAAACTATTGGAACTGTCATCTGAGCANA
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Pred. No. 2.6e-29;
0; Mismatches 95
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (484)
; OTHER INFORMATION: r
US-10-008-118A-5
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US-10-008-118A-5
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SEQ ID NO 5
LENGTH: 514
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (484)
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                                                                                                                                                  TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 USDIV
CURRENT APPLICATION NUMBER: US/10/008,118A
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/109,294
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 514
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Best Local Similarity 66.2%;
Matches 227; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cahoon, Rebecca E. APPLICANT: Weng, Zude
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                                                                                                          TYPE: DNA
ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 GAAAAACTATTGGAACACTAATCTTCTAAGGAAGTTAAATACT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 CTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGT
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2636
LENGTH: 774
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
IITLE OF INVENTION: STRESS-REGULATED GENES OF PL
TITLE OF INVENTION: SAMB, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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Best Local Similarity 66.2
Matches 227; Conservative
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 222; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-938-842A-2636
                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                  152 GTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACATATCAAGAGAGGTGACTTTGAAC 211
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GTTGTAGATTGAGATGAATTATCTAAGACCAGATCTCAAAAGAGGCAATTTTACTG
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GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: US 60/300,111
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SEQ ID NO 2636
LENGTH: 774
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2636
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Search completed: January 30, 2004, 09:31:32 Job time: 304 secs
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US-09-938-842A-2636
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                                                                                                                                           332 TTCTAAGGAAGTTAAATACTACTAAAATTGTTCC 365
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                                                                                                          TCAAGAGGAAGCTTCTCAGCCGTGGGATTGATCC
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

253.2 252.2 252.6 196.8	% Query Score Match
30.7 30.6 27.0 23.9	Query Match
490 418 335 749	Query Match Length DB ID
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490 10 BE462282 418 9 AW626121 335 10 BE462229 749 13 BQ990780	SUMMARIES
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Result No.

142.2 17.2 633 14 CA90248	142.4 17.3 491 14 CD48026	.6 17.3 721 10 BG12	142.8 17.3 549 13 BU81256	1 143.4 17.4 645 13 BU81656	0 143.6 17.4 505 12 BM52888	9 144.4 17.5 548 12 BJ5	8 145.4 17.6 857 10 BF26994	7 146.6 17.8 452 9 A	6 147 17.8 468 14 CB92274	5 147.6 17.9 737 13 BU89179	4 148.2 18.0 671 10 BG44782	3 149 18.1 475 9 AW18	2 149.6 18.1 572 9 1	1 150.2 18.2 757 12 BGE	0 150.2 18.2 671 13	9 150.6 18.3 646 14	8 150.6 18.3 355 9	7 151.4 18.4 797 13	6 151.4 18.4 656 9	5 151.4 18.4 642 12	4 151.4 18.4 617 9 AI73064	3 151.4 18.4 522 12	2 151.6 18.4 505 14 CA9024	1 151.8 18.4 562 9	0 151.8 18.4 447 9	9 153 18.5 620 9	8 153 18.5 579 9 1	7 154.6 18.7 574 14	6 154.6 18.7 447 10	154.8 18.8 636	4 155.2 18.8 781 13	3 157.4 19.1 397 12	2 165.4 20.0 587 14	165.6 20.1 494 14	165.8 20.1 551 12	172.2 20.9 508 13	.2 20.9 488 13 BQ10504	172.2 20.9 427 13	184.4 22.4 486 9 A	185 22.4 367
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## ALIGNMENTS

FEATURES source	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BE462282 LOCUS DEFINITION
Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence. Location/Qualifiers 1490	F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, 0-3 mm buds Unpublished Contact: CUGI	Lycopersicon esculentum  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  1 (bases 1 to 490)  van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang	Lycopersicon esculentum cDNA clone cTOA12C2, mRNA sequence. BE462282. BE462282.1 GI:9508051 EST. Lycopersicon esculentum (tomato)	BE462282 490 bp mRNA linear EST 18-MAY-2001 EST324546 tomato flower buds 0-3 mm, Cornell University

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REFERENCE
AUTHORS
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Lycopersicon esculentum cDNA clone
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Email: http://www.genome.
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/dev gtage="0-3mm buds"
/clone_lib="comato flower buds 0-3 mm, Cornell Universit
/clone_lib="comato flower buds 0-3 mm, Cornell Universit
/note="Vector: pBlueScript SK(-); Site_l: EcoRl; Site_2:
Xhol; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
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organism="Lycopersicon"
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                                                                                                                                                                                                                   Lycopersicon esculentum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 335)

van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.

Generation of ESTs from tomato flower tissue, 0-3 mm buds
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                                                                                                                                             Clemson University
                                                                                                                                                                                   Unpublished
Contact: CUGI
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                                                                                                         Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                              100 Jordan Hall,
                                                                                                                                                                Clemson University Genomics Institute
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xhol; supplier: Tanksley; Tissue supplied
(USDA-ARS, Ithaca, NY 14850)."
79 c 91 g 119 t 1 others
/organism="Lycopersicon
/mol_type="mRNA"
/cultivar="TA496"
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                                                                                                                              SC 29634, USA
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JOURNAL COMMENT
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SOURCE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ATAAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGGAAAATGGCATCTTGTTCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                            1 (bases 1 to 749)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Klain, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ990780
QGF21B10.yg.ab1 QG_EFGHJ
QGF21B10, mRNA sequence.
BQ990780
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] singleton, see http://cgpdb.ucdavis.edu/ for details. plate: QGF21 row: B column: 10.
                                                                 Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactuca sativa
                                                                                                                                                                                                                                      http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                           Cichorieae; Lactuca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ990780.1 GI:22410315
                                                                                                                                                                                           Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGATGTGAAGAACTATTGTGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATAAGCTCTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCCGGAAGGACAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev stage="0-3mm buds"
/dev stage="0-3mm buds"
/clone_lib="tomato flower buds 0-3 mm, Cornell University"
/note="Vector: pBlueScript SK(-); Site_1: EcoRl; Site_2:
Xho1; supplier: Tanksley; Flower buds_and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

size-separated while remaining frozen."
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/clone="cTOA12C3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="flower"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Matches 246; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 TACTACTACTCATGGTTTAGGATTAAGAAAAGGTGCATGGACTGCACATGAAGATACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        442
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                                                                                                                                                                                                                                                                                BF635572 367 bp mRNA linear EST 19-DEC-2000 NF104H01DT1F1014 Drought Medicago truncatula cDNA clone NF104H01DT 5', mENA sequence.
BF635572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TACATCTATGTCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCT
Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                          Medicago truncatula
                                                                                                          Medicago.
                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                            BF635572.1 GI:11899730
                                                                                                                                                                                                                  Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAAACTATTGGAACACTAATCTTCTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAGGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTAAGAAAATGTATTGATAAGGTATGGTGAAGGAAAATGGCATCTTGTTCCCATAAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTAGGCAACAGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGAACTACTGGAACACAAATATTCAA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTGAGGCTTCATAAGCT
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                                                                                      (bases 1 to 367)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias: Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB-QG_EFGHJ lettuce serriola
TAG_TISSUE=leaves dark grow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAG_SEQ=GCTAGTCGGG"
129 c 157 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="L.serriola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Lactuca sativa"
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Pred. No. 3.6
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                                                                Bell, C.J.,
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Plant Biolo
The Samuel
2510 Sam No
Tel: 580 22
Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillnan, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: gdmay@noble.org
Insert Length: 367 Std Error: 0.0
Plate: 104 row: H column: 01
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                        A1995124 486 bp mRNA
701502113 A. thaliana, Ohio State clone
CDNA clone 701502113, mRNA sequence.
                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; euroside II, Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 486)
                                                                                                                                 Arabidopsis thaliana (thale cress)
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AI995124.1
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It Biology Division

Samuel Poundation

Samuel Roberts Noble Foundation

Sam Noble Parkway, Ardmore, OK 73402,

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580 221 7380
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/tissue_type="Plantlets"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/clone_lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of entire
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1. .367
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/mol_type="mRNA"
/db_xref="taxon:3880"
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   Fragrance-Related Genes
Plant Cell 14 (10), 232
Contact: Naama Menda
                                                                                                                                                                                                              BQ105368
BQ105368.1 GI:20155030
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: service@genomesystems.com
Location/Qualifiers
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/db_xref="taxon:3702"
/clone="701502113"
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Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134. Hear Tel: 877-2733
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                                                                                                                                                                                                                  Rosa hybrid cultivar
Rosa hybrid cultivar
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, roside,
eurosids I; Rosales, Rosaceae, Rosoideae, Rosa.
                                                                                                   1 (bases 1 to 427)
Guterman, I., Shalit, M., Menda, N., Piestun, D., Dafny-Yelin, M., Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J., Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and W
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                                                 Rose Scent: Genomics Approach to Discovering
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/note="cDNA library was made from selected clones from the
Arabidopsis thaliana Ohio State clone set."
a 83 c 111 g 144 t
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Fax: 972 8 9468 263
Guterman,I., Shalit,M., Menda,N., Piestun,D., Dafny-Yelin,M., Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J., Z., Pichersky,E., Lewinsohn,E., Zamir,D., Vainstein,A. and W
                                                    Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophy
Spermatophyta; Magnoliophyta; eudicotyledons; cor
; eurosids 1; Rosales; Rosaceae; Rosoideae; Rosa.
1 (bases 1 to 488)
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hybrid cultivar cDNA clc
BQ105048.
BQ105048.1 GI:20154710
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Seq primer: T3 forward.
                                                                                                                                                          Rosa hybrid cultivar
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/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap
Express Library"
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82 c 111 g 92 t
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/strain="Fragrant Cloud"
/db_xref="taxon:128735"
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A. and Weiss
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Rosa hybrid cultivar
Rosa hybrid cultivar
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosid
                                                             BQ104423

g90628.e Rose Petals (Golden Gate) Lambda hybrid cultivar cDNA clone gg0628.e 5', mR BQ104423

BQ104423.1 GI:20154085

EST.
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Tel: 972 8 9489 389
Fax: 972 8 9468 263
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Seq primer: T3 forward.
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The Hebrew University of Jerusalem
P.O. Box 12, Rehovot, 76100, Israel
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Rose Scent: Genomics Approach
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/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Golden Gate) Lambda
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/strain="Golden Gate"
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/clone="gg1664.e"
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                                BM092559 ST 29-NOV-20 Sah15d11.y3 Gm-c1086 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1086-1342 5' similar to TR:023891 023891 OSMYB3. ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Faculty of Agricultural, Food and Environmental Quality Sciences, The Hebrew University of Jerusalem P.O. Box 12, Rehovot, 76100, Israel
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                                                                                                                                                                                                                                                                                                              GCTTCCGGGGAGGACTGGTAATGATGTGAAGAACTATTGGAATTGTCACTTGAGCAAAAA
                                                                                                                                                                                                                                                                                                                                          ACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTATTGGAACACTAATCTTCTAAGGAA 341
                                                                                                                                                                                                                                                                                                                                                                                                                GGATCTCATTTTGAGGCTTCATAAGCTCTTAGGCAACAGATGGTCACTTATTGCTGGTAG
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                                                                                                                                                                                                                                                                        GTTAAATACTACTAAAATTGTTCCTCGCGAAAAGATTAACAATAAGTGTGGAGAAATTAG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAATGTATTGATAAGTATGGTGAAGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCATGGACTAAGGAAGAGGATCAGTTGCTGAGGAAATGCATAGAGAAGTATGGAGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        il: shaham@agri.huji.ac.il
primer: T3 forward.
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972 8 9468 263
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92 c 137 g 109 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Golden Gate) Lambda Zap Express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .508
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/clone="gg0628.e"
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/strain="Golden Gate"
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Pred. No. 2.1e-23;
0; Mismatches 118;
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          South Memorial Parkway Huntsville, AL 35801 For further is call: (800)-533-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Public Soybean EST Project
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
GCCACATATCAAGAGAGGTGACTTTGAACAAGATGAAGTGGATCTCATTTTTGAGGCTTCA
                                                                                                                     AAGAGCTGGTCTGAATAGATGTCGGAAAAGTTGTAGATTGAGGTGGCTGAATTATCTAAG
                                                                                                                                                                           GAGAAGCCCTTGTTGTTCAAAGGAGGGTTTGAATAGAGGTGCTTGGACAGCTCATGAAGA
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//INCLEST/YORD SMITCAGE
//INCLEST/YORD SMITCAGE
XhoI; The cDNA library was constructed from mRNA isolated from very young seeds (less than 20mgs). The library was prepared using the Stratagene pBluescript II SK (+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an Xho I restriction site. Eco RI adaptors were ligated to the blunt-ended cDNA fragments followed by Xho I digestion. The cDNA insert is protected from Xho I digestion via methylation during first strand cDNA sythesis. The cDNA fragments were directionally cloned into the Eco RI-Xho Irestriction site of the pBluescript vector. The ligated cDNA fragments were pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cell. The library was constructed by Anu Khanna (Lila Vodkin lab, University of Illinois)."
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'tissue type="young seeds (Williams 82)"
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Pred. No. 3.6e-22
0; Mismatches 11:
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SOURCE
ORGANISM
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843_F -P proteoid r
5', mRNA sequence.
CA410578
19 TCTTCATTGGGAGTGAGAAAAGGTTCATGGACTGATGAAGAAGATTTTCTTCTAAGAAAA 78
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Mylon filter arrays reveal differential gene expression roots of white lupin in response to P deficiency Unpublished (2003)

Contact: Unde-Stone, Claudia

Department of Agronomy and Plant Genetics
University of Minnesota
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: AATTAACCCTCACTAAAGGG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lupinus albus (white lupine)
Lupinus albus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 612 624 6765
Fax: 612 625 2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uhde-Stone,C., Zinn,K.E., Ramirez-Yanez,M., Li,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cuhde@soils.umn.edu
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                                                                                                                                                           /dev stage="12 and 14 DAE"
//dev stage="12 and 14 DAE"
//dev stage="12 and 14 DAE"
//clone lib="-p proteoid root (cluster root); Vector:
//note="Organ: -p proteoid root (cluster root); Vector:
pBLUESCRIPT SK(+/-); Site 1: EcoRI; Site 2: KhoI; Proteoid
roots of white lupin grown under p deficient conditions
were harvested 12 and 14 DAE (days after emergence); and
poly(A)+ RNA was isolated. The poly(A)+ RNA obtained from
plants 12 and 14 DAE was combined in a 1:1 ratio and 7 ug
total RNA was used for reconstruction of a proteoid root
cDNA library in the phage ZAPII vector according to the
manufacturer's instructions (Stratagene, La Jolla, CA, USA
). For conversion of the phage library into the plasmid
form, mass excision was performed according to the
procedure described by Stratagene."
197 a 71 c 111 g 96 t 19 others
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                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:3870"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="ultra"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Lupinus albus"
                                                                                     20.1%;
                                                                                     Score 165.6; DB 14; Pred. No. 3.9e-22;
                                                                   Mismatches
                                                                 142;
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                                                                                                      Length
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MSU-DOE Plant Research Laboratory
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                     Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
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1 (bases 1 to 587)
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Tel: 517-353-0854
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,E. and Somerville,C.
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/note="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not; /note="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and
                                                                                                                                                                                                                                                                                         /organism="Arabidopsis/mol_type="mRNA"
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                                                                                                                                                                                        /clone_lib="Lambda-PRL2"
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                                                                                                                                                                                                                                                               strain="var columbia"
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                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterstron, R. and Wilson, R., Pape, D., Harvey, N., Schurk, R., Waterstron, R. and Wilson, R., Waterstron, R. and Wilson, R., Public, Soybean EST Project
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BG881996 GHycine max CDNA CIONE SYSTEMS
ID: Gm-c1065-3356 5' similar to TR:Q40920 Q40920 MYB-LIKE
TRANSCRIPTIONAL FACTOR MBF1. ;, mRNA sequence.
                                                                                                 Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max
                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway,
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a 106 c 135 g 167 t 14 others
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID:
                                                            organism="Glycine max"
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                                                                                                                                                                                                                                                                                          Box 8501, St. Louis, MO
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Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea,
Tel: +46 90 786 5279
Fax: +46 90 786 6676
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Contact: BHALERAO RUPALI R.
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neberg, P., Bhalerao, R.R.,
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BU827658
                                                                                                              Tal: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.
Location/Qualifiers
                                                                                                                                                                          Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea,
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/db xref="taxon:47664"
/tissue type="apical shoot"
/clone lib="Populus apical shoot cDNA libxary"
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/organism="Populus tremula x Populus
/mol_type="mRNNA"
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/tissue_type="apical shoot"
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                                                                      | AC011613 Drosoph | AP003707 Oryza s<br>AC092848 Homo sa | AF262040 Arabido                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | AC0905                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | AP0028<br>AC1307                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  
                                                                                                                                                                                                                                                                          | AC101180 Mus musi | AC125434 Homo sa;<br>AP004936 Lotus i                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | AL353757 Human Di                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | AC111159 Homo sa                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | X92945<br>AL1617                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | AX0595                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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AX346247   Sequence   482   1832   8   18 2.2   20315   1 AE014280   AE014280   Streptoco   483   18 2.2   20315   1 AE014280   AE014280   Streptoco   483   18 2.2   20315   1 AE014280   AE01541   Drosophil   484   18 2.2   20313   8   AE014280   AE01541   Drosophil   484   18 2.2   20313   AE014280   AE01541   Drosophil   484   18 2.2   20313   AE014280   AE01541   AE014280   AE01541   AE014280   AE01541   AE015 | ## ADDITION AND PROPERTY OF THE PROPERTY OF TH | A05 18 2.2 15951 6 AX346583 AX346583 Sequence 478 18 2.2 7995 2 406 18 2.2 15951 6 AX348806 AX346806 Sequence 479 18 2.2 80074 9 18 2.2 16931 1 AE001716 AE002138 Dreaplasm C 480 18 2.2 80074 9 18 2.2 16931 1 AE001716 AX346806 Sequence C 480 18 2.2 80074 9 18 2.2 16931 1 AE001716 AE002138 Dreaplasm C 480 18 2.2 80074 9 18 2.2 16931 1 AE001716 Thermotog C 481 18 2.2 81172 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 403 18 2.2 15972 9 AC09594 AC09594 AC09594 AD000 sapi C 476 18 2.2 79643 2 405 18 2.2 15951 6 AX346583 AX346583 AX346583 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2.2   8207   10   PMUID22467   ALT22467   Mus muscu   C 467   18   2.2   75468   395   18   2.2   10227   1 ARD06438   ACL10793   Home sapi   468   18   2.2   77688   396   18   2.2   10227   1 ARD06438   ACL10793   Home sapi   469   18   2.2   77708   3970   18   2.2   10256   1 ARD01645   ARD06438   Lactococci   469   18   2.2   77708   398   18   2.2   10256   1 ARD01645   ARD01645   ARD06438   Lactococci   470   18   2.2   77729   399   18   2.2   10256   1 ARD01764   ARD01766   ARD01766   ARD01764   ARD01766   ARD01766 | 18 2.2 6611 1 BSARLMNP M292467 | 1990   18   22   5540   8 ANDST788   ANDST | 188   18   22   5002   14 ARSY7296   APSY5296 Casphalia   461   18   22   71912   18   22   55640   ABO57788   BC046423   ABO57788   APSO2042   ABO57788   APSO2042   APSO2042 | 18               | 188                                   | 1882   188   2.2   3767   9 AR094510   AP094520   AP0 | 18               | 10                                   | 377 18 2.2 318 9 AKOO7643 ARICOT643 Home 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protein (an2) mRNA, an2-S9 allele,
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AC100811 Homo sapi
AC128084 Rattus no
AL645770 Homo sapi
AP001125 Homo sapi
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AL161502 Arabidops
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AC109540 Rattus no
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AC009561 Homo sapi
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Petunia integrifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Petunia.

1 (Dases 1 to 865)
1 (Dases 1 to 865)
Ouattrocchio,F., Wing,J., van der Woude,K., Souer,E., de Vetten,N.,Mol,J. and Koes,R.
Molecular analysis of the anthocyanin2 in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
                                                                              Petunia integrifolia
Petunia integrifolia
Petunia integrifolia
Rukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
1 (bases 1 to 866)
Quattrocchio, F., Wing, J., van der Woude, K., Souer, E.,
Quattrocchio, F., Wing, J., van der Woude, K.,
                                                                                                                                                                                                                                                                                                                   Petunia integrifolia An2
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1087, Amsterdam 1081HV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quattrocchio, F., W
Mol, J. and Koes, R.
Direct Submission
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                                                                  L,J. and Koes,R.
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LNRCKKSCRLRWLNYLRPHIKGGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGKTAND
VKNYWNTHLRKKLIAPHDQKQESKNKAMKITENSIIKPRTFSRPAMHVSCWNGKS
CNKNYTIDKNEGDTEIIKFGDEKGKPERSIUDGLQWWAANLLANNIEIEELVSYNSPTLL
HEETAPSVNAESSLTQEGGGGLSDFSVDIDDIWDLLS"
133 c 193 g 229 t 1 others
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/protein_id="AAF66728.1"
/db_xref="GI:7673086"
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/allele="an2-S9"
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/chromosome="6"
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/cultivar="S9"
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Pred. No.
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eudicots;
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Quattrocchio,F., Win
Mol,J. and Koes,R.
Direct Submission
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10449578
                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Ssterridae; lamiids; Solanales; Solanaceae; Petunia.

1 (bases 1 to 868)

Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.
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Petunia x hybrida An2 truncated
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Submitted (29-APR-1999) Genetics, Vrije Universiteit, 1087, Amsterdam 1081HV, Netherlands Location/Qualifiers
                                                       Quattrocchio, F., W. Mol, J. and Koes, R.
                                                                                                                                  Mol,J. and Koes,R.
Molecular analysis of the anthocyanin2
in the evolution of flower color
Plant Cell 11 (8), 1433-1444 (1999)
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Petunia x hybrida
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                                           Direct Submission
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                                                                                       (bases 1 to 868)
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134 c 195 g 227 t
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/db_xref="GI:7673088"
/db_xref="GI:7673088"
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/translation="MSTSWASTSGVRKGAWTEEEDLLLRECIEKYGEGKWHLVPVRAG
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/translation="MSTSWASTSGVRKGAWTEEEDLLLRECIEKYGEGKWHLVSCWNGKS
VKNYWNTHLRKKLIAPHDQKQESKNKAMKITENNIIKPRQTFSRPAMMHVSCWNGKS
VKNYNTIDKNEGDTEIIKFSDEKQKPEESIDDGLQWWANLLANNIEIEELVSCNSPTLL
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'chromosome="6"
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Pred. No.
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1 (bases 1 to 1034)
Colorio, F., Wing, J., van der Woude, K., Souer, E., Colorio, Colorio, Wing, J., van der Woude, K., Souer, E., Colorio, 
                                                                                                                                                                                                                                                                                                                                  Submitted (29-APR-1999) Genetics,
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LNRCRKSCRLRWLNYLRPHIKRGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGRTAND
VKYVWNTHLRKKLIAPHDQKQESKS"
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/replace="nnnn"
                                                                                                                                               organism="Petunia
/mol_type="mRNA"
/cultivar="V26"
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/gene="an2"
                               tissue_type="petal limb" . .1034
                                                                                          /db_xref="taxon:4102"
/chromosome="6"
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db_xref="GI:7673092"
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                            Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg
10, Koeln D-50829, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             Werber, M., Stracke, R. and Weisshaar, B. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1339)
Stracke, K., Werber, M. and Weisshaar, B.
The R2R3-MYB gene family in Arabidopsis thaliana
Curr, Opin. Plant Biol. 4 (5), 447-456 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                            Submitted (18-APR-2001) Dept. Plant Breeding and Yield Physiology
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ilarity 100.0%;
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LNRCRKSCRLBWLNYLRPHIKGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGRPAND
VKNYMNTHLRKKLIAPHDQKQESKNKAPKITENNIIKPRPRTFSRPAMNIFPCWNGKS
CNKNTIDKNEGOTEIIKESDEKQKPEESIDDGLGWAANLLANNIEIEELVSCNSPTLL
HEETAPSVNAESSLTQGGGSGLSDFSVDIDDIWDLVS"
/translation="MGRAPCCEKIGLKRGRWTAEEDEILTKYIQTNGEGSWRSLPKKA
GLLRCGKSCRLRWINYLRRDLKRGNITSDEEEIIVKLHSLLGNRWSLIATHLPGRTDN
EIKNYWNSHLSRKIYAFTAVSGDGHNLLVNDVVLKKSCSSSSGAKNNNKTKKKKKKKGRT
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/protein_id="AAF66727.1"
/db_xref="GI:7673084"
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                                          /product="putative transcription factor"
/protein_id="AAK97396.1"
/db_xref="GI:15420626"
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                                                                                                             /gene="At5g49330"
/note="ATMYB111; R2R3-MYB family member"
                                                                                                                                                             /gene="At5g49330"
                                                                                                                                                                                                                                           organism="Arabidopsis
mol_type="mRNA"
db_xref="taxon:3702"
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Address for correspondence: kaos@kazusa.or.jp
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
Inttp://www.kazusa.or.jp/Kaos/cgi-bin/agd_graph.cgi?c=MIF21
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
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                                                                                                                                                                    This sequence may not be the entire insert of this clone. It may shorter because we remove overlaps between neighboring submission The 5' clone is MDN11 and the 3' clone is K23F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-PBB-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
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DNA Res. 7 (1), 31-63
20181125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H.
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Arabidopsis thaliana
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DIGEITLE"
                             /mol_type="genomic DNA"
/strain="Columbia"
                                                                                organism="Arabidopsis thaliana"
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/chromosome="5" /clone="MIF21"

clone\_lib="Mitsui Pl"

exon	exon	exon	exon	exon	exon	exon	exon	exon	exon	exon	exon	exon
/number=7 /evidence=not_experimental complement(544445503)	/number=8 /number=8 /evidence=not_experimental complement(\$062, .5250) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown_protein"	unknown protein" /number=9 /evidence=not_experimental complement(49104963) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21	complement (43674453)  /note="CDS is reported in Acc# AB017064  gene id:MDN11.21	unknown protein"  /number=11 /evidence=not experimental /evidence=not experimental complement(35614266) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein" /number=10 /evidence=not experimental	/number=12 /number=12 /number=10 /evidence=not_experimental /evidence=not_experimental complement(30333412) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21	/number=13 /evidence=not experimental complement(28312952) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 publications	unknown protein"  /number=14 /evidence=not experimental complement(21612266) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein"	/number=15 /number=15 /number=16 /evidence=not_experimental /evidence=not_experimental complement(12732061) /note="cDS is reported in Acc# AB017064 gene_id:MDN11.21	/number=16 /number=16 /evidence=not experimental complement(770845) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein"	/number=17 /number=17 /evidence=not_experimental /evidence=not_experimental complement(587. 698) /note="CDS is reported in Acc# AB017064	unknown protein"  /number=18  /evidence=not experimental  complement(109263)  /note="CDS is reported in Acc# AB017064  gene_id.MDN11.21  unknown protein"	<pre>complement(130) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21</pre>
CDS			CDS			CDS	exon	exon	exon	. exon	exon	
complement(join(1411214562,1464715668)) /note="gene_id:MIF21.4"	NEAC CE E LOS L WILESCH NUMBE CASE IN CHIMSE IN PARTICULAR IN CHIMSE CASE IN CALL STATE IN A CHIMSE CASE IN THE STATE OF THE CASE IN CASE IN CASE IN CASE IN THE STATE OF THE CASE IN	/ Godon start=1 / Godon start=1 / evidence=not_experimental / protein_ide_"spalacturonase" / protein_ide_"shaya694.1" / db_xref="GI:8777404" / translation="MGRVHFGVSAFFVFCLLGLSANAKIFNINSPPGSDITNALLKAF / translation="MGRVHFGVSAFFVFCLLGLSANAKIFNINSPPGSDITNALLKAF / translation="MGRVHFGVSAFFVFCLLGLSANAKIFNINSPPGSDITNALLKAF	complement (join (1052210773,1092511443,1152411826, 1191412027)) /note="gene id-MTF21 3"	WSEDILIVSRCIESIAFTACMEILDPERRREKPVIMLERWNQPWEYTNIERIINOT WIKDLTDLPFEFFKKIIGSLRRGGMKERVYSPLVALYASKSVIPEGQTNTDILQRALD LLLTRDKAYRFVPVGFYFACLANDLKHDTVLKLQDQIVSLLHTAQPENFIYPKAGNRQ VAFSQELLTMESLFSVVVSTESERHLTSSSSNVRVGKLMDIFLSRLPYDQEMKTTRFI ELIETVPMSFRESHDQLYLAVNAFLQHTNISQEEKGSICSYLNCQKLSQEASLELVK NEKMPLALVVQALFIQQLNTHQAFKUCSDSFRFTNSADFSGSVVPSSRPLTS9QSPCT DDETGPRNRPLCFLMQKDATLDEFESTSFRIHNLEEQLVSLKKSLHSHDNLKKPNCLG KRSASRNKNTFGQVTTACIGSVSFTSQRKYANRLLQILRRVNLFGSRKTNRSKAGESE PI	/ evidence=not_experimental /protesin_ide=BA96993_1" /db_xref="GI:8777403" /db_xref="GI:8777403" /translation="METFSLKDCSSVASSPISSPNISTLLKIKVLSWSKETGLPASVH /translation="METFSLKDCSSVASSPISSPNISTLKIKVLSWSKETGLPASVH VRVCNKSFNLHKSLLCAKSGYFKERBOOLSBIEIPOBFPGGAETFBKIMLFIYGCPTL IHPFNIAGLRCAAQFLEMTEQHSTGNLCERFDLYLNQVVLQNWDDTLVVLKKCQDLVP	ntain IIF21 art=1	/number=2 /evidence=not_experimental complement(63156389) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein"	/ Humber	/ number - 1 / evidence=not_experimental complement(60356089) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein"	/ Number - 1 / evidence=not experimental complement (58595936) /note="CDS is reported in Acc# AB017064 gene id:MDN11.21 unknown protein"	/number=6 /evidence=not_experimental /evidence=not_experimental complement(56035790) /note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein"	/note="CDS is reported in Acc# AB017064 gene_id:MDN11.21 unknown protein"

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             Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, X., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox., Coyle, M., Cree, A., D'Souza, I., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Denamo, C., Dingy, Dinh, H., Divya, K., Delgado, O., Denson, S., Denamo, C., Dingy, Dinh, H., Divya, K., Delgado, O., Denson, S., Dunn, A., Dubhin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabis, A., Ganta, R., Garcia, A., Garrer, M., Gebregeorgia, E., Geer, K., Gill, R., Grady, M., Guerra, M., Gebregeorgia, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hadun, S. L., Hodgson, A., Hogues, M., Hernandez, J., Hanes, S., Hlayk, S., Hamil, C., Hamilton, K., Jackson, A., Jokeson, A., Honderson, M., Hogues, M., Hernandez, J., Hanes, S., Hadun, S. L., Hodgson, A., Hogues, M., Guarra, W., Guarathy, S., Kally, S., Kally, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kaft, C.L., Lebow, H., Lovan, J., Lewis, L., Liz, T. Liu, J., Liu, J., Lewis, L., Lebow, H., Lovan, J., Lewis, L., Liz, T. Liu, J., Liu, J., Lewis, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mayman, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martin, C., Martin, K., Martin, R., Martin, S., Munghy, M., Norris, S., Nunghy, M., Norris, S., Nunghy, M., Norris, S., Nunghy, M., Norris, S., Nunghy, M., Norris, S., Parks, K., Paster, M., Sedergten, S., Scott, C., Primus, E., Pu, L., L., Paster, M., Sedergten, S., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shen, J., Shen, J., Shen, J., Shen, J., Shen, J., Walton, R., Watter, M., Watte, R., Watte, A., Tabox, P., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Storella, R., Sosa, S., Dumn, D., Voon, V., Walter, B., Wang, J., Walter, B., Wang, J., Walter, B., W
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23; Conserv
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved
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Center clone name: CH230-15207
Center clone name: CH230-15207
Center clone name: CH230-15207
Center Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 223122 bases at least Q40
Consensus quality: 224872 bases at least Q30
Consensus quality: 225979 bases at least Q20
Consensus quality: 225979 bases at least Q30
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end_sequence:BH336082"
30867. .33254
/note="wgs_end_extension
                                                                                                                                             /note="clone_boundary
clone_end:T7
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clone_end:Sp6
site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                            clone="CH230-15207"
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                                                                                                                                                                                                                                       sequence:BH336083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type="genomic DNA"
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 19, 2002 this sequence version replaced gi:21745861.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 232747)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                        Center: Baylor College of Medicine Center code: BCM
http://www.hgsc.bcm.tmc.edu/
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1 (bases 1 to 865)

Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.
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Petunia axillaris An2 truncated
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-APR-1999) Genetics, V. 1087, Amsterdam 1081HV, Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol, J. and Koes, R. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular analysis of the anthocyanin2 gene of petunia and its role in the evolution of flower color
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clone_end:T7"
38121_.39480
/note="wgs end_extension
clone_end:T7"
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34423. .38020
/note="nonsense mutation"
/replace="c"
136 c 195 g 229
                                                                        /translation="mSTSNASTSGVRKGAWTEEEDLLLRECIEKYGEGKWHLVPVRAG
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VKNYWNTDLRKKLIAPHD"
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/protein_id="AAF66734.1"
/db_xref="GI:7673098"
/db_xref="GI:7673098"
                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                            'gene="an2"
                                                                                                                                                                                                                                                      'gene="an2"
                                                                                                                                                                                                                                                                     'tissue_type="petal limb"
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                                                                                                                                                                                           note="anthocyanin regulator; myb-related transcription
                                                                                                                                                                                                                                      allele="an2-S7"
                                                                                                                                                                                                                                                                                               db_xref="taxon:33119"
chromosome="6"
                                                                                                                                                                                                                                                                                                                              cultivar="87"
                                                                                                                                                                                                                                                                                                                                                        organism="Petunia axillaris"
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100.0%; Pre
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1 (bases 1 to 868)

Quattrocchio, F., Wing, J., van der Woude, K., Souer, E., de Vetten, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-APR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol, J. and Koes, R. Direct Submission
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Quattrocchio, F., Wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular analysis of the anthocyanin2 gene of petunia and its role in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
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                                                     Similarity
TGAATTATCTAAGGCCACATAT 191
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LNRCRKSCRLRWLNYLRPHIKRGDFSLDEVELILRLHKLLGNRWSLIAGRLPGRTAND
VKNYWNTHLRKKLIAPHDQKQESKS"
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137 c 195
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/allele="an2-W44"
                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:4102"
chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                    note="anthocyanin regulator; myb-related
                                                                                                                                    note="causes frameshift leading
                                                                                                                                                                                                                                                                                                                                                                tissue_type="petal limb"
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Pred. No.
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Pred. No.
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                                                                  Length 868;
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                                                                                                                                                                                                                                                                                       transcription
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AC097536 Homo sapiens BAC clone AC097536 AC032034
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Mol, J. and Koes, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-APR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular analysis of the anthocyanin2 gene of petunia and its role in the evolution of flower color Plant Cell 11 (8), 1433-1444 (1999)
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lnrcrkscrlrwlnylrphikrgdfsldevelilrlhkllgnrwsliagrlpgrtand
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/note="causes frameshift leading
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note="anthocyanin regulator; myb-related transcription
                                                                                                                                                                                                                                                                                                                                                                                           allele="an2-W115"
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                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="petal limb"
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chromosome="6"
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cultivar="W115"
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                                                                                                                                               Score 22;
Pred. No.
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Submitted (18-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                 Direct Submission
Submitted (12-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Feb 9, 2002 this sequence version replaced gi:16902008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cedroni, M., Haglund, K. and Creason, K.
The sequence of Homo sapiens BAC clone
Unpublished (2001)
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HTG.
                                                                                                                                                                                                                                            MO 63108, USA
5 (bases 1 to 194553)
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Waterston, R.H.
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Sulston, J.E. and Waterston, R.
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           Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Conter: Summary Statistics
Center project name: H_NHO803N05
Drafting Center: WIBR
                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
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Missouri 63108,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

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FEATURES
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Location/Qualifiers
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Rattus norvegicus clone CH230-39011, WORKING DRAFT
ACL30926
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 15, 2002 this sequence version replaced gi:23264859. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-AUG-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 219481)
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KEYWORDS
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                                           AC103077.5 GI:25188654
HTG; HTGS-PHASE1; HTGS_DRAFT;
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                 AC103077 220494 bp DNA linear HTG 23-N Rattus norvegicus clone CH230-224J5, WORKING DRAFT SEQUENCE,
Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                           AC103077
                                                                                                                                                              unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)
NOTE: This is a "working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
                                                                                                                                                                                                                                                                                                                               AGAAGATGAAGAGGTTGTAATT 126595
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1 219481: contig of 219481 bp
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Assembly program: Phrap; version 0.990329
Consensus quality: 213455 bases at least Q40
Consensus quality: 213451 bases at least Q30
Consensus quality: 215564 bases at least Q20
Estimated insert size: 224277; sum-of-contigs estimation
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a 42948 c 42163 g 60766 t
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/db_xref="taxon:10116"
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                On Nov 23,
The sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-NOV-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separate by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
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RESULT 14
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Haemophilus influenzae Rd
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NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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a 43966 c 42534 g 58135 t
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6265. .8020
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6264: gap of unknown length
216851: contig of 210587 bp in length
216951: gap of unknown length
218096: contig of 1145 bp in length
218196: gap of unknown length
218196: gap of unknown length
219224: contig of 1028 bp in length
219324: gap of unknown length
219324: gap of unknown length
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                                                                                                                                                                                                                                                                                                               Score 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Hayes,W.S., Borodovsky,M., Rudd,K.E. and Koonin,E.V. Metabolism and evolution of Haemophilus influenzae deduced from whole-genome comparison with Escherichia coli Curr. Biol. 6 (3), 279-291 (1996)
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White,O., Clayton,R.A.,
Peterson,J., Hickey,E.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. I expressed and a number of frame shifts have been corrected. I we have gratefully acknowledge the work of Tatusov et. al. We have incorporated their annotation into the /notes fields of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-SEP-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Fleischmann. New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (bases 1 to 10913) White,O., Clayton,R.A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-JUL-1995) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 10913)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ical Center Dr, Rockville, MD 20850, USA whole genome was shifted by 588 nucleotides for a new that 1, 196 this sequence version replaced gi:1221866. Location/Qualifiers
                                                                              /translation="mfklksvnlqvyimliaiavimaffsvatdgaylsarnisnllr
QTSITGXLAIGMVFVIISAEIDLSVGSLMGLLGGFAAIADVMGGFPLFVTIIATIALG
LIFGIWGMWVAYRKVPSFIVTLAGYLAFRGILIGLTNGTTVSPISGTMTVIGQGYSL
DIAGVILGGIAVIGFVLMGNYQRRSRQQLQLEVSALSKDFTKYALFAVIVLGAIYLLA
DYRGIPFPVLVLAVLAILGLFLSRKTSFGRHVYAIGGNIDAAKLSGINVEKTKLIIFA
                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SP:P37389 PID:466706 GB:U00096 PID:1789992 percent identity: 69.81; identified sequence similarity; putative"
                             MNGVLVAIAGLILSARLGAGSPSAGQNAELDAIAACVIGGASLAGGVGSVFGVVIGAL
IIASLDNGMSMLDVPTFWQYIVKGGILLLAVWIDTSNKKKM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (168. .1295)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Haemophilus influenzae
/mol_type="genomic DNA"
/db_xref="laxon:71421"
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                                                                                                                                                                                                                          /protein_id="AAC22763.1"
/db_xref="GI:1574663"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="HI1109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .10913
                                                                                                                                                                                                                                                                                                           product="D-xylose ABC transporter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="HI1109"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kerlavage, A.R. and Fleischmann, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kerlavage, A.R. and Fleischmann, R.D.
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GFNFDAKIRRQSIDPYDLFYAHIGAIDVLALSLÄRAAKMLQEETLQKIVNERYAGWNS
ELGQHILQGKTSLETLAQLVQQKDLAPKPVSGQQEYLENLVNQVIYS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mttyfdkiekisfegekstnpfafkhydanqviigktmaehlrl
Ancymhtfcungkndhgelselerswormsklagabokadiafelekiklgvpyycfhd
VDIAbegnsvreyvqnfhilvdilerkqvetgkkelmghancftnprymsgaatnpnp
Evfamaatqvfnlagatgenyvlmggregyftlntdlkrebroigermghqmve
HXHKIGFKGTLLIEPKPQEPTKHQYDYDVaTVYGFLKQFGLEKEIKVNIEANHATLAG
HTFQHEIATACALDIFGSIDANRGDPQLGMDTDQFPNSVEENTLVMYEILKHGGFTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity, putative"
/codon_start=1
/transT_table=11
/product="xylose isomerase (xylA)"
/protein_id="AAC22766.1"
/db_xref="GI:1574666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mkiksalltivgaltvesssahskdikiglsiddlrleerwokdr bievnkaesmgakvevogsangddsagisolerminnknidulvi ephogevlsnvisea kkegikvlaydeltnadldevyspeneroeglaksivavkpegnyelmokggspydnn aklerkgomkvldpliasgkikvvodowvosmlaekalginenaltaanknudavvas ndataggalohlsaggisolohaaikrivngsotmtvykpitkladkaae iavelgknenaltaakkalgkaae
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/transl_table=11
/product="D-xylose ABC transporter, periplasmic-binding
protein (xylp)"
/protein_id="AAC22765.1"
/db_xref="GI:1574665"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVGTKDASTMTEDDIITMMVGREITSLYPHEPHEIKDEILRVENLSAMHPINTHIKRV
DNVSFSLHEGEILGVAGLVGSGRTDMVGCLFGSYEGKREGNIEINGKOVNIKNCAQAI
EHKIVMVPEDRKKHGIVSIMGVGKNITLASIKASYCFGKMVVNWEAKEEQIIGSAIKRK
VKTFSPDLPIGRLSGGNQQKAILAKCLSLNPKILILDEPTRGIDVGAKYEIYKLINQL
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/gene="HI1110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:1789990 percent identity: sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2861. .3859)
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LGNEITHKGLTADNEMYLRCKNLLQQVQLDADPNTRVGELGLGQQQLVEIAKALNKQV
RLLILDEPTASLTEKETEILLNLIKDLKAHNIACIYISHKLNEVKAISDKICVIRDGE
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/trānslation="MKQKCGCIPPHFFILGDIMYIGIDCGTQGTKAIVLDSVQKKVIG
VGYAKHELITQSNGRREQQPNWWIEALQQALQIALKQAKNSPHFSPNLVKGIGISGQQ
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                                                              /product="xylulose kinase"
/protein_id="AAC22767.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GB:X04691 SP:P00944 GB:K01996 GB:S68257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="HI1112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP:P37387 PID:466704 GB:U00096
PID:1789990 percent identity: 75.99; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="HI1111"
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                                                                                                                                                              /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                dentified by sequence
                                                                                                                                                                                                                                                                                                                                                                   'gene="HI1113"
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db_xref="GI:1574664"
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table=11
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                                                                                                                                                                                                                                                                      note="similar to
                                                                                                                                                                                                                                                                  PID:2293419 percent identity: 52.56;
                                                                                                                                                                                                                            similarity; putative"
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Research, 9712

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                                                             Hardwight Franciscon Francisco Franci
                                   Utterback, T., McDo
Venter, J.C. et al.
Complete genome se
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum section AE001227 AE000520 AE001227.1 GI:3322797
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8594. .9265
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LDIADYCDKEDFIASIIAGDERGDIDAVFHEGACASTTEWDKYIMHNYYEYSKELLH
YCLDREIFFFYASSAATYGDTKVFREBREFEGPLNVYGYSKFLFDQYYRHILFBAKSF
VCGFRYFNVYGPRENHKGSMASVAFHLNNOILKGENFKLFAGSEHFRDFVYVGDVAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGLVMLDKNDR PLYKAKLWCDTETATENDILIEKLGGQTAVFEKLGIICQTGYTASKL
SWFRQNY PDKFANIRKIMLPHDYLNYWLTGKFCTEFGDASGGSVEDVVKKEWKREVFK
YLAPELNMDEVLPKLLSAEQKIGVIKDEIATLFGFNENVIVSTGGGDNWGAICTGNU
REGIATMSLGTSGTLYAYTQKPLLNLPPMIANFCSSNNGWLPLVCVMNITSSNKQLMN
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QGNTFSLESLDQNKFTLLYFWGTWCGYCRYTSPAINSLAKEGYQVVSVALRSGNEADV
NDYLSKNDYHFTTVNDPKGEFAERWQINVTPTIVLLSKGKWDLVTTGLTSYWGLKVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to PID:1213065 SP:P52229 percent ide
36.36; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (7980. .8483)
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ADLTKLRSTGYDKPFKTVAEGVTEYMAWLNRK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (7001.
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EAAALGGAIQAMWANGEGELEFLCETFIHLDENSKAYPNLSQVKNYQNAYERYLTHLS
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/protein_id="AAC22769.1"
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/transl_table=11
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/protein_id="AAC22768.1"
/db_xref="GI:1574668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-MAR-1998) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 281 (5375), 375-388 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MELOKKETALAOSOVELEVVVAREDAORHYORFVEEYLERARLP
GFRKGKVPLAVLERKYGSAIROPAAALMEKALEEGFRQASOOSED 15 RPSZLEKYTE
VPDPDEDFSRAVIIYVFFPSVELRNTSGFSLSVYEVTVSVTEEDVSRELTRIOERNALVTD
KGADSCAEVGDIATVDYHEVDDSGAVRPGTERAGVVFTLGVEBGPFALGODILGMKLG
GRCLFARRAGMLKDEAAQVRVTLKALKGRQLESLDDELAQDVSDAFRTLDDLTRSVRQ
URLEALEAALHEYKRROLLRILVERBEPFSLPESLVVEGMESUMALVNROGFOUSLSGTB
URLABALEAALHEYKRROLTRILVERBEPFSLPESLVVEGMESUMALVRROGFOUSLSGTB
ONKLOFFQOMRPEVEEHLKGRVIVEILLKQEQVSVSAEEIETEYVRIASKTGSKEERV
/trānslation="mrerminlvpyvieqsggersydifsrllkdriifvdgeitda
vadlvvaqllflesgnrekdislyinspegavvaglavydtmglicpevqticleqas
smaavllaggapegkrealessrvminlppmgevqqqasbvciqaqeilrlktititayfa
lhtgqseeqvredmerdfflsaeqacsygivdtvmkkrkqaqv"
                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:L42023 SP:P43867 PID:1005637
PID:1220799 PID:1204962 percent identity: 60.42;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="trigger factor (tig)"
/protein_id="AAC65494.1"
/db_xref="GI:3322798"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REYYAGEEKRRALCEGIRERKLCQKLLGRCVTECGPEQSLTDFLQEQSRA =
                                                                                                                                        /protein_id="AAC65495.1"
/db_xref="GI:3322799"
                                                                                                                                                                                                                                                /product="ATP-dependent Clp
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/transl_table=11
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="similar to GB:AE000783 percent identity: dentified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="TP0508"
2505. .3752
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PASSVLISAKTGENVDALFDAIITRIPPPQGSGTAALQALVFDCHYDQYRGVVVHIRV
FEGQVTSGMVIRFMSNGAEYRVEETGVFVFNLIAREALCAGDVGYLSANVKTVSDVQV
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3849. .4415
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ALFALDDVRL VFDEDALDA I AQQA I DQKTGARGLRS I VERLMLDAMFEA PSLKGKKEL
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IDSVLIEKSNVLLIGPTGSGKTLLAKTLSQKMKVPFAIADATTLTEAGYVGEDVENIL
LKLVQNANGDVALAERGIIFIDEIDKISRKSENVSITRDVSGEGVQQALLKIIEGTIA
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identified by sequence similarity; putative"
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Search completed: January 30, 2004, 10:14:24 Job time: 2286 secs
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Leqrasepaltrgisvlpcteegalryglgtdmhalcagrplliagihlpskkcaqgh
sdadvlahasidallgaaglgdigtffpscdgrwkdahscallrhtwqlvraacwrlv
Nldavycleqpalhpfreawraslaqaldthvtrvfvkaktaerlgpvgsgaavtaqv
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PID:606224 percent identity: 23.86; identified by sequence
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                                                                                                                                       esculentum
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              GAAGAAGATGAAGAGGTTGTAATTAATTATGAAAAAACACTAACAAGTTTGTTACATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes tomato anthocyanin 1 (ANT1). The ANT1 polynucleotide can be used for modifying the expression of a native plant gene, particularly for producing an anthocyanin 1 bhenotype in plants, which is responsible for many red and blue colours in plants. The polynucleotide is useful for modifying e.g. leaf colour, flower colour or fruit colour in plants. The present sequence represents an ANT1 genomic DNA fragment which is used in an example from the present ANT1 genomic DNA fragment which is used in an example from the present and the present and the present sequence represents and the present and the presen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide derived from tomato, useful for producing an Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf color, flower color or fruit color in plants -
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AACAATAAGTGTGGAGAAATTAGTACTAAGATTGAAATTATAAAACCTCAACGACGCAAG
                                                                                                             TGGAACACTAATCTTCTAAGGAAGTTAAATACTACTAAAATTGTTCCTCGCGAAAAGATT
                                                                                                                                                        TGGAACACTAATCTTCTAAGGAAGTTAAATACTACTACTAAAATTGTTCCTCGCGAAAAGATT
                                                                                                                                                                                                                                                                                                 AGATGGTCACTTATTGCTGGTAGACTTCCCGGAAGGACAGCTAACGATGTGAAAAACTAT
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                                                                                                                                                                                                                                                                                                                                                                            68.7%; Score 567; DB 24; ilarity 100.0%; Pred. No. 3.6e-273; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield;
          Pilgrim
                                                                                                                                                                                                                                                                                                                                                   (MEND-)
(PILG/)
(CREE/)
(DUBE/)
(HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-2000;
16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK65274 standard; cDNA; 1300
                                                                                                                                                                                                                (KEDD/)
(ADAM/)
(RATC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001;
                                                                                                                                                                                                                                                                                                                       (JIAN/)
                                                                                                                                                                                    (REUB/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yield;
                                                                                                          ADAM L.

RATCLIFF O.

REUBER J L.

RIECHMANN J L.

YU G.
                                                                                                                                                                                                                                                                         HEARD J.
JIANG C.
KEDDIE J.
          Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                               CREELMAN R.
DUBELL A J.
                                                                             PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATATTGGTGAAGGTAACTCCATGCAACAAGGACAAATAAGTCATGAAAATTGGGGTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding a transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-227439P.
; 2000US-0713994.
; 2001US-0837944.
       Creelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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          Dubell
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          Heard J,
          Jiang
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          Ç
              Keddie J;
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985 798 925 738 865 678 805 618 745 558 685 498 625

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AAAO1109/c

ID AAAO1109 standard; cDNA; 30

XX AAO1109;

XX 19-MAY-2000 (first entry)

XX Human colon cancer cell lir

XX Human; colon cancer; tumous

KW Human; colon cancer; tumous

KW probe; detection; cancerous

KW breast cancer; oestrogen receptor-negativ

XX Homo sapiens.

XX W09958675-A2.

XX PD 18-NOV-1999.

XX PD 18-NOV-1999.

XX 11-MAY-1998; 98US-008542

PR 11-MAY-1998; 98US-008553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc readable medium having stored sequence information, and identifying a cc homologue sequence from a database comprising a plurality of known plant cc sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or crecombinant polynucleotide is used for producing a plant having a condified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the colynucleotide or antisense nucleic acid, inserting the colynucleotide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color polypeptide or antisense nucleic acid, thereby producing a modified color production of agriculturally useful proteins or metabolic chemicals, color polypeptide or antisense nucleic acid, thereby producing in the proteins or metabolic chemicals, color polypeptide or antisense and many other traits listed in the conscious and the proteins or metabolic chemicals and color polypeptide or antisense research sequence is one of the 232 polypucleotides or anceptical proteins or metabolic chemicals and color polypeptide or antisense research sequence is one of the 232 polypucleotides or anceptical proteins or metabolic chemicals.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer
                                                                                                                                                                                                                                                                                                                Human; colon cancer; tumour; diagnosis; gene expression produc probe; detection; cancercous state; metastasis; identification; breast cancer; estrogen receptor-positive breast cancer; ther oestrogen receptor-negative breast cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 523-525; 941pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1300 BP; 392 A; 210 C; 350 G; 348 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human colon cancer cell line polynucleotide sequence SEQ ID NO:1100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-292022/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAACAGATGGTCACTTATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A. thaliana transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
           98US-0085426.
98US-0085537.
                                                                                                 99WO-US10602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC genes correlated with a cancerous state of a mammalian cell, comprising cc detecting at least one differentially expressed gene product in a test complete derived from a cell suspected of being cancerous, where detection confidence is correlated with a cancerous state of the cell from which the test sample was derived. CC The polynucleotides sequences can be used in a method for detecting confidentially expressed genes correlated with a cancerous state of a confidential cell. The polynucleotides can also be used as probes for cc mammalian cell. The polynucleotides can also be used as probes for cc detecting and mapping related genes. They can be used in diagnosis and congruents of diseases and disorders (e.g. identification of cresponsiveness of cancer to therapy). This is particularly for breast cc cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-concer, and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reinhard
Lamson G,
                                                                                                                                                       arthritis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                                                                                                                                                                                                                      Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #2452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 300 BP; 128 A; 44 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-126369/11.
                                                                                                                                            antiasthmatic;
                                                                                                                                                                                                      cellular fucosylation; glycoconjugate
                                                                                                                                                                                                                                                                                      10-FEB-2003
                                                                                                                                                                                                                                                                                                                                                 ABX20395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed
                                                15-AUG-2002.
                                                                              US2002110548-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                       GDP-mannose 4,6-dehydratase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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d C, Giese K,
G, Drmanac R,
itz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 445; 1097pp; English.
                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAAGTGGATCTCATTTTGA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAGTGGATCTCATTTTGA 176
                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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98US-0105234.
98US-0105877.
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Randazzo F, Kennedy GC,
Crkvenjakov R, Dickson M,
Garcia V, Jones LW, Sta
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                          GM4,6D; gene; ss; inflammation; e fucosylation; transplant reje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stache-Crain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac
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                                                                                                                                                                                                          rejection;
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11-JUN-2001; 2001US-0878574.

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RESULT 6
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ID AAA024
XX AAA024
XX 19-MAY
XX 19-MAY
XX Human
XX Human;
KW probe;
KW breast
KW oestro
XX Homo s
XX Homo
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Best Local S
Matches 21
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03-DEC-1997;
09-SEP-1998;
14-JUN-1999;
  14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or amellorating diseases affected by the level of cellular fucosylation or diseases affected by the level of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding human GM4,6D peptides of the invention.
                                                                                                                                                                                                                                                                                                                         probe; detection; cancerous state; metastasis; identification;
breast cancer; oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                     Human;
probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets screening GM4,6D antagonists for treating e.g. arthritis, or tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA02459
                                                                                                              13-MAY-1999;
                                                                                                                                                                   18-NOV-1999.
                                                                                                                                                                                                                      WO9958675-A2
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to a composition comprising a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 GATGTGAAAAACTATTGGAAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; cDNA; 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer cell line polynucleotide sequence SEQ ID NO:2450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           cancer; tumour; diagnosis; gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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97US-0984246.
98US-0149674.
99US-0333177.
  98US-0085426.
98US-0085537.
98US-0085696.
                                                                                                              99WO-US10602
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAA00010 to AAA02716 represent polynucleotides isolated from cDNA CI libraries constructed from human colon cancer cell lines. The present colintration also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising conferentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting conferentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for cetecting and mapping related genes. They can be used in diagnosis and corrects of diseases and disorders (e.g. identification of cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                       07-JUN-1995;
21-APR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
                                                                                                                                                                                                                                                                        Haemophilus
                                                                                                                                                                                                                                                                                                                         expression modulating fragment; regulation;
organism; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                          Genome; bacterium; Haemophilus influenzae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae complete
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27-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON COR
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; 1830121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAAGTGGATCTCATTTTGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      765 BP; 298 A; 123 C; 136 G; 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 982; 1097pp;
                                                                                                                                                                                                                                                                          influenzae
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                       95US-0487429.
95US-0426787.
95US-0476102.
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98US-0105877.
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Randazzo F, Kennedy GC, I
Crkvenjakov R, Dickson M,
Garcia V, Jones LW, Stav
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                                                                                                                                                                                                                                                                                                                                              gene expression;
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4, Drmanac
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RESULT 8
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XX ABZ1
AC ABZ1
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XX AFABZ1
XX AFABZ1
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                                                                                                                                                                                                                                                                                                                                                                   24-AUG-2000;
26-JAN-2001;
22-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae Rd genome medium - useful for identifying fragments by homology searching
                                                                                                                                                                                     WPI;
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                                                                                                 Identifying a stress condition to which a plant cell has been and producing plants with increased tolerance to these abiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-AUG-2001; 2001WO-US26685
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                                                                                                                                                                                                                                      Harper JF,
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(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
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07-MAY-1999;
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14-0CT-1999; 99US: 14-0CT-1999; 99US: 18-0CT-1999; 99US: 21-0CT-1999; 99US: 22-0CT-1999; 99US: 22-0CT-1999; 99US: 25-0CT-1999; 99US:	10-SEP-1999; 99US- 13-SEP-1999; 99US- 15-SEP-1999; 99US- 20-SEP-1999; 99US- 22-SEP-1999; 99US- 23-SEP-1999; 99US- 24-SEP-1999; 99US- 24-SEP-1999; 99US- 26-SEP-1999; 99US- 27-SEP-1999; 99US- 28-SEP-1999; 99US- 28-SEP-1999; 99US- 29-SEP-1999; 99US- 29-SEP-1999; 99US- 21-OCT-1999; 99US- 11-OCT-1999; 99US-	10-AUG-1999; 99US- 11-AUG-1999; 99US- 12-AUG-1999; 99US- 13-AUG-1999; 99US- 13-AUG-1999; 99US- 16-AUG-1999; 99US- 17-AUG-1999; 99US- 20-AUG-1999; 99US- 20-AUG-1999; 99US- 20-AUG-1999; 99US- 21-AUG-1999; 99US- 23-AUG-1999; 99US- 23-AUG-1999; 99US- 24-AUG-1999; 99US- 25-AUG-1999; 99US- 25-AUG-1999; 99US- 27-AUG-1999; 99US-	27-JUL-1999; 99US- 27-JUL-1999; 99US- 27-JUL-1999; 99US- 28-JUL-1999; 99US- 02-AUG-1999; 99US- 02-AUG-1999; 99US- 03-AUG-1999; 99US- 04-AUG-1999; 99US- 04-AUG-1999; 99US- 05-AUG-1999; 99US- 05-AUG-1999; 99US- 06-AUG-1999; 99US- 06-AUG-1999; 99US- 06-AUG-1999; 99US- 06-AUG-1999; 99US- 06-AUG-1999; 99US- 06-AUG-1999; 99US- 09-AUG-1999; 99US- 09-AUG-1999; 99US-
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XX Antib
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25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                  The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
                                                                                                                                           anti-Listeria vaccines.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; SEQ
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                                                                                                Sequence 684707 BP;
                                                                                                                                                                                                                                                   treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria innocua contig DNA sequence #9
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                                                                                                                                                                                                                                                infections by Listeria,
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2.4%; Score 20; DB ilarity 100.0%; Pred. No. 9. Conservative 0; Mismatches
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99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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99US-0161406.
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99US-0161360.
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100.0%; Prr
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                           DB 24;
9.4;
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                                                                                                  211468 T; 3 other;
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RESULT 12
AAK62944/c
ID AAK629
XX

AAK62944 standard;

CDNA; 464

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(first entry)

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RESULT 11
ABG69245/c
ID ABG692
XX ABG692
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XX Antiba
XW Infect
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XW Infect
XX Lister
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XW 11-APR
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Best Local Similarity
                                                                                                                                                                                                                                             Sequence 3011208 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                     (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators -
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                                                                                                                                                                                                                                                                                                                                                                                              anti-Listeria vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID 2058; 180pp; French.
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                                  TAATCTTCTAAGGAAGTTAA 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
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08-DEC-2000; 2000US-0251990.

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05-JAN-2001; 2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                         Bone marrow; diagnostic; therapeutic; gene therapy; antigenic; haematopoiesis; myeloid; lymph cell disorder; tissue regeneration; wound healing; nutritional supplement; immune disorder;
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Plasmodium falciparum

05-NOV-1998; 05-NOV-1999; 11-MAY-2000

98US-0107131. 99WO-US26796. 07-NOV-2000 AAA70171;

(first entry)

AAA70171 standard; DNA; 810

ВP

Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide; ds. Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:304.

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Conappropriate bone marrow polypeptide expression by rectifying mutations of deletions in a patient's genome that affect the activity of the copypeptides by expressing inactive proteins or to supplement the activity of the copypeptides by expressing inactive proteins or to supplement the actids may be used to produce the polypeptides, by inserting the nucleic complements of culturing the cell to express the protein.

Consider any be used to produce the polypeptides, by inserting the nucleic complementary sequences may also be used as DNA complementary sequences may also be used as DNA complementary and therefore which patients may be in need of restorative therapy. The proteins may also be used as complementary and therefore which patients can in assays to identify modulators of their expression and activity. The antibodies may also be used as complementary and antagonists may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate apents for detecting the presence of the protein seamples (e.g. by enzyme linked immunosorbant assay (ELISA)). The proteins complement of mysloid or lymph cell disorders in tissue regeneration, such as wound healing; as a nutritional supplement; and in treatment of immune disorders such as severe combined immunodeficiency (SCID).
Sequence 737 BP; 232 A; 112 C; 182 G; 191 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS22907-AAS23099 represent nucleic acids encoding novel bone marrow polypeptides. The nucleic acids and corresponding proteins may be used in the prevention, diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 162; 392pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor; biochemical characteristic; controlling structural characteristic; developmental characteristic; gene agricultural biotechnology; plant trait modification; ss.
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Search completed: January 30, 2004, 09:36:34 Job time : 282 secs

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Best Local Similarity
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                                                                                                                Sequence 1137 BP; 378 A; 213 C; 233 G;
                                                                                                                                                                                                                                                                                                                 The present sequence is Arabidopsis thaliana transcription factor, G1324 cDNA. The transcription factor is used for altering a plant's biochemical characteristics. The transcription factor may be used to alter the structure and developmental characteristics of plants such as alter the structure and developmental characteristics of plants such as
                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding plant for altering the biochemical potato and cotton plants -
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Pilgrim M, Pineda O,
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17-APR-2000;
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AV674350 AV674350
BZ660408 WHABDSTF
AV976001 AV976001
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BY756830 BY56830 BY756830 BY75680 
BJ082401 BJ082401
BB491490 db71f06.x
BU743442 mai31h08.
BU19124 zb15c02 r1
AJ499746 AJ499746
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                                                                          medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 Contact: Dixon RA
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Fax: 580 221 7380
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NF103E12EC1F1097 Elicited cell culture Medicago truncatula cDNA
Clone NF103E12EC 5', mRNA sequence.
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                                                                                                                                     Email: radixon@noble.org
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Plate: 103 row: E column: 12
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                       Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                        Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7302
                                                                                                                                                                                                                                                                                                                        Contact: Dixon RA
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days. Cells were induced six days after subculture"
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tissue_type="Cell cultures derived from root tissues"
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  185
                          175 TATCTAAGGCCACATATCAAGAGAGGTGACTTTG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE462229 335 bp mRNA linear EST 18-MAY-2001 EST324493 tomato flower buds 0-3 mm, Cornell University Lycopersicon esculentum cDNA clone cTOA12C3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 Jordan Hall, Clemson, SC 29634, USA
=mail: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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BE462229
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                                                                                                                                                                                                   /tissue_type="flower"
/dev_stage="0-3mm buds"
/dev_stage="0-3mm buds"
/clone_lbe="tomato flower buds 0-3 mm, Cornell University"
/clone_lbe="tomato flower buds 0-3 mm, Cornell University"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
sze-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture" /clone_lib="Elicited cell culture" /note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 at 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation." a 122 c 128 g 183 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4081"
/clone="cTOA12C3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Lycopersicon
/mol_type="mRNA"
/cultivar="TA496"
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BE462282.1 G
                                                                                                       1 (bases 1 to 490)
van der Hoeven, R. S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, 0-3 mm buds
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W.,
Fraser,C.M., Matrin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato radicle tissue (etoliated)
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1 (bases 1 to 418)
                                                                 Unpublished Contact: CUGI
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100 Jordan Hall, Clemson,
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EST.
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79 c 91 g 119 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University"
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/dev_stage="seedlings 5 days post-imbibition"
/clone_lib="tomato radicle, 5 d post-imbibiti
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                             Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF519256 245 bp
EST456718 DSIL Medicago truncatula
                                                                                                                                                                                                                              Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M276687e
TIGR sequence name: MTFCE77TK
More information is available at: http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.Holt,I.E. and Fraser,C.M.
ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fedorova, M., Pierson, B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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651 649 5058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="flower"
/dev_stage="0-3mm buds"
/clome_lib="tomato flower buds 0-3 mm, Cornell University"
/clome_lib="tomato flower buds 0-3 mm, Cornell University"
/clome="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

93 c 105 g 136 t
/dev_stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
                                                           trifolii"
                                                                                                                 /mol_type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:4081"/clone="cTOA12C2"
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|mol_type="mRNA"
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                                                                                                 |one="pDSIL-20M9"
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                                                                           type="leaves infected with Colletotrichum
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1e-06;
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Craven, M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inductory:
1 (bases 1 to 367)
1 (bases 1 to 367)
1 Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble For Expressed Sequence Tags from the Samuel Roberts Noble For Madingon truncatula drought library
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; rosids
Spermatophyta; Magnoliophyta; eudicotyledons; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     College Division
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
ON 73402, USA
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                                                                                                                                                                                                                                                                                                                                                                                 Plate: 104 row: H column: 01
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: gdmay@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: May GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note| Colletor: pBluescript Stratched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletor: chum trifolii. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells. Note: EST may
be of fungal origin."
74 a 32 c 66 g 73 t
                                                                                                         142 a
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                                                                                                       timepoints.
                                                                                                                                          /clone_lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of enti-
plantlets harvested in a series of days-post-watering
                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                              dev_stage="Pooled timepoints"
                                                                                                                                                                                                                                                        clone="NF104H01DT"
                                                                                                                                                                                                                                                                              db xref="taxon:3880"
                                                                                                                                                                                                                                      tissue_type="Plantlets"
                   3.3%;
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Pred. No.
                     Score 27;
Pred. No.
                                                                                                         85
  Mismatches
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0.0058;
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                                       Length 367
                                                                                                         4 others
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clone NF104H01DT
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    <u>,</u>
                                                                                                                                                                         of entire
    Gaps
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142 TGTCGGAAAAGTTGTAGATTGAGGTGG 168

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RESULT 9
BF006562
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BF006562 526 bp mRNA linear EST 06-OCT-EST435060 DSLC Medicago truncatula cDNA clone pDSLC-42B13, mRNA
                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              More information is available at. . http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fedorova, M., Pierson, B.L.,
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Medicago truncatula
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EST391494 GVN Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 Borlaug Hall, 1991 Upper Buford Circle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        truncatula
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: vance004@maroon.tc.umn.edu
                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                  183
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651-649-5058
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,I.E. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                     /note=TVector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised
                                                                                                                                                                                                                                                                                                          from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."
75 c 108 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E._coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype A17"
/cultivar="genotype A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="N2-fixing root nodules"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="pGVN-30E12"
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                                                                                                                                                                                                                           Score 27; pred. No.
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                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                               0.0067;
                                                                                                                                                                                                                                                     DB 10;
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                                                                                                                                                                                                                                                Length 526;
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                                                                                                                                                                                                                                                                                                                238 AGTTGTAGATTGAGGTGGCTGAATTAT 264
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BF006562
BF006562.1
                                                                                                                                               sequence.
BE124179
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M275600e TIGR
MTLBEO7TK More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
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Fax: 651 649 5058
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ESTs from Medicago truncatula leaves and cotyledons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                         BE124179.1
EST.
                                                                                                                                                                                          EST394304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Plant Pathology University of Minnesota
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                                                              Medicago truncatula
                                                                                     Medicago truncatula (barrel
                                                                                                                                                                                                           BE124179
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                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=TVector: pBluescript SK +/-; Site 1: EcoRI; Site 2: XhOI; cDNA was prepared from polyA+ enriched RNA from the mixture of cotyledons of five days old plants and leaves of two weeks old plants. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="leaves and cotyledons"
/dev stage="mixture of cotyledons from fiv plants and leaves obtained from two weeks /lab host="E. coli strain SOLR"
/clone_lib="DSLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant lambda-ZAP phage using Ex-Assist helper phage
and propagated in SOLR cells."
98 c . 110 g 127 t
                                                                                                                                                                                      DSIL Medicago truncatula
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/mol_type="mRNA"
/cultivar="genotype_A17"
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/clone="pDSLC-42B13"
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                                                                                                                                                                                      near EST 07-SEP-2000
pDSIL-13E12, mRNA
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eks old plants"
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  JOURNAL
                      TITLE
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                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                             381 AGTTGTAGATTGAGGTGGCTGAATTAT 407
                                                                                                                                                                                                                         sequence.
BG588067
BG588067.1
BST.
                                                                                                                  Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
Spermatophyta; Magnoliophyta; Pabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: debbys@puccini.crl.umn.edu
Minnesota sequence name: M262137e
TIGR sequence name: MTFH10TKB
More information is available at..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 1243
Fax: 651 649 5058
ESTs from phosphate-starved roots of Medicago truncatula, 2001
Unpublished
                                                                                                                                                                                                                                                                                                    BG588067
EST489876 MHRP- Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Deborah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fedorova, M., Pierson, B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 549)
                                     Harrison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTTGTAGATTGAGGTGGCTGAATTAT 177
                                                                               (bases 1 to 585)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.3%; So ilarity 100.0%; I Conservative 0;
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//Clone_lib="DSIL"
//Clone="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
//nore="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
//nore="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
//nore="Vector: prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was directionally ligated into the Uni-ZAP XR vector from directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chrysie.tamu.edu/medicago
imer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="leaves infected with Colletotrichum trifolil"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E__coli strain XLOLR"
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/clone="pDSIL-13E12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; ; Pred. No.
                                                                                                                                                                                                                                                                                                  585 bp mRNA linear EST 12-APR-2001 truncatula cDNA clone pMHRP-41C11, mRNA
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0.0068;
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                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 618)
Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Vai
Utterback,T., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula treated with
oligogalacturonides of DP 6-20
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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The Samuel Roberts Noble Foundation: N266740e TIGR sequence name:
MTHAI18TKB More information is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 580-223-5810
Fax: 580-221-7380
                                   Tel: 706-542-4457
Fax: 706-542-4412
                                                                                                                  University of Georgia
220 Riverbend Road, Athens,
                                                                                                                                                                                                          Contact: Michael G. Hahn
Complex Carbohydrate Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula (barrel medic)
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Seq primer: SKmod (CTA c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Biology Division
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Email: hahn@ccrc.uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTTGTAGATTGAGGTGGCTGAATTAT 177
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/note="Vector: pBluescript Sk-; Site_1: EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; EcoRI; EcoRI; EcoRI; EcoRI; EcoRI; EcoRI; EcoRI
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/mol_type="mRNA"
/cultivar="A17"
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lab_host="XLOLR"
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Pred. No. 0.0069;
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cDNA clone pHOGA-18G24
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                                                                                                                                     G390832e TIGR sequence name: MTMBW30TK More information available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Utterback,T., Cho,J. and Fraser,C.M. ESTs from roots of Medicago truncatula treated with oligogalacturonides of DP 6-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula (barrel medic)
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EST508845 HOGA Medicago truncatula cDNA clone pHOGA-16E11 5' end,
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                                                                                                                                                                                                                Email: hahn@ccrc.uga.edu
                                                                                                                                                                                                                                                                          220 Riverbend Road,
                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                       Michael G. Hahn
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/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"
/lab_host="XIOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The was directionally ligated into the Unizap XR vector fr
                                                         /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
tissue_type="3 day old seedling roots"
                    /db_xref="taxon:3880"
/clone="pHOGA-16E11"
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/mol_type="mRNA"
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0.0071;
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                                                                                                                                                                                                                                                                                                                 241 CATAAGCTCTTAGGCAACAGATGGTC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 AGTTGTAGATTGAGGTGGCTGAATTAT 258
BU876538 308 bp mRNA 1
V021H11 Populus flower cDNA library Populus
trichocarpa cDNA 5 prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 781)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 bp mRNA T008E08 Populus apical shoot cDNA library tremuloides cDNA 5 prime, mRNA semisario EURA 12 prime prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +46 90 786 5279
Fax: +46 90 786 6676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: BHALERAO RUPALI R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from multiple libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unneberg, P., Bhalerao, R.R., Jan
The poplar tree transcriptome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Populus tremula x Populus tremuloides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTTGTAGATTGAGGTGGCTGAATTAT 177
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//note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."

a 124 c 132 g 172 t
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/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Populus tremula x Populus
/mol type="mRNA"
/db_xref="taxon:47664"
/tissue_type="apical shoot"
/clome_lib="Populus apical shoot cDN/
147 c 183 g 181 t
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Pred. No.
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Pred. No.
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0.0072;
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0.027;
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Populus tremula x Populus
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AUTHORS
TITLE
Search completed: January 30, 2004, 10:47:17 Job time : 2028 secs
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ORIGIN
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source
                                                                                                                                                                           Query Match 3.0%; Score 25; DB 13; Best Local Similarity 100.0%; Pred. No. 0.066; Matches 25; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhaleraogplantphys.umu.se.
Location/Qualiflers
Tel: 1. .308
                                                                                                                 590 ATGACGATATTGAAGAAGATGAAGA 614
                                                                                          139 ATGACGATATTGAAGAAGATGAAGA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Populus balsamifera subsp. trichocarpa
Populus balsamifera subsp. trichocarpa
Populus balsamifera subsp. trichocarpa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malphyhiales; Salicaceae; Populus.

1 (bases 1 to 308)
Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished
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BU876538.1 GI:24068062
EST.
                                                                                                                                                                                                                                                                                     /organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub species="trichocarpa"
/db_xref="traxon:3694"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"
75 c 59 g 86 t
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                                                                                                                                                                                                                      Length 308;
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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Result
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Maximum DB
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AAU75735
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Arabidopsis thalia
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	AAU92995	23	371	5	374	5
Arabidopsis thalia	AAE01913	22	371	25.3	374	44
Myb-related transc	ABJ10416	23	273	ŗ	374	ü
	AAB68353	22	280	5	375	2
w	5	21	280	5	375	11
	$\mathbf{r}$	23	268	<u>ب</u>	377	0
	24	22	274	5	7	39
dopsis	129	21	274	5	77	8
	AAB67842	22	236	5	75	37
	AAG49909	21	236	ŗ	7	8
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đ	ABJ10408	23	258	Ģ	75	4
elated tr	ABJ10422	23	246	٥.	œ	ພ
radiat	AAB33306	21	255	٥.	87	32
related	ABJ10420	23	253	٥.		μ
lyptus gr	AAB33239	21	153	٥.	38	ö
related	ABJ10409	23	120	٥.	393	29
Myb-related transc	ABJ10412	23	302	٥.	396.5	8
dopsis tr	AAU93088	23	342	٥,	397	27
radiata	AAB33283	21	176	?	399.5	8
ta	AAB33044	21	148	7.	400	25
psis trans	AAU93131	23	203	7.	401	24
Ø	AAB82482	22	226	?	402.5	23
thali	AAG30441	21	257		403	22
ca.	AAG30442	21	246	7.	403	21
Arabidopsis thalia	AAG29947	21	278		408	õ
	AAE02486	22	269	7.	408	9
8	AAG29948	21	269	.7	408	8
dopsis	AAG29949	21	258	7	408	17
gra	AAB33293	21	205	8	415	6
s radiata tra	AAB33304	21	391	28.4	420	5
_	248	22	302		422	
o	835	22	211	4.	510	ω
ß	9317	23	209	5	518.5	Ņ
s thali	0193	22	209	35.1	7	F
Arabidopsis transc	AAU93155	23	212		524	5

## ALIGNMENTS

RESULT 1

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N-PSDB; ABQ73046.	WPI; 2002-557819/59.	Conners K, Mathews HV, Liu A;	(EXEL-) EXELIXIS PLANT SCI INC.		30-OCT-2000; 2000US-244685P.		29-OCT-2001; 2001WO-US50638.		18-JUL-2002.		WO200255658-A2.		Lycopersicon esculentum.		Tomato; ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour.		Tomato anthocyanin 1 (ANT1) protein SEQ ID NO:2.		24-SEP-2002 (first entry)		ABB81626;		ABB81626 standard; Protein; 274 AA.	1626

36.1 36.1 36.1

Arabidopsis Arabidopsis A. thaliana

transc thalia Produc

XEEE

New isolated polynucleotide derived from tomato, useful for producing an Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf color, flower color or fruit color in plants

Amino acid sequenc Arabidopsis thalia Arabidopsis transc A. thaliana Produc

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ARESULT 2
AREO1932
ID AREO
XX AREO
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Matches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                               17-NOV-1999;
17-APR-2000;
22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription factor; trait modification; structural characteristic; developmental c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE01932 standard; Protein;
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(MEND-)
(REUB/)
(CREE/)
(PILG/)
(RIEC/)
(JIAN/)
                                                                                                                                                                                                                                                                14-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agricultural biotechnology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana transcription factor homologue G2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2001
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) PILGRIM M.
) RIECHMANN J L.
) JIANG C.
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                                                                                            MENDEL BIOTECHNOLOGY INC. REUBER L.
                                                                     CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HENWGEFSLNLPPMQQGVQNDDFSAEIDLWNLLD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fruit colour in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 AA;
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2000US-0197899.
2000US-0227439.
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Pred. No. 1.9e-133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                characteristic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seed characteristic;
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RESULT 3
AAU93177
ID AAU93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify phremyl lipid content, to modify fatty acid and modify wax content. They may also be used to alter seed characteristics such as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reuber i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding plant transcription factor polypeptides, if for altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants -
                                                                                    Agriculture; metabolic chemical; environmental stress; microbial disease resistance; herbicide resistance; see fruit yield; growth rate; leaf senescence; flower senes
                                                                                                                                                                               02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription factor G663. The transcription factors may modify traits associated with structural or developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 114; 133pp; English
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N-PSDB; AAD05767.
                                           Arabidopsis thaliana.
                                                                                                                                               Arabidopsis transcription factor #215.
                                                                                                                                                                                                                                        AAU93177
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(PINE/) PINEDA O.
(HEAR/) HEARD J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLN----TTKIVP
                                                                                                                                                                                                                                        standard; Protein;
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                                                                                                                                                                                                                                                                                                              CNKDEQKDKLININLLDGDNMWWESLLE
                                                                                                                                                                                                                                                                                                                                         C-KEIISEKQTPDASMDNVDPWWINLLE 194
                                                                                                                                                                                                                                                                                                                                                                                                   REKINNKCGEISTKIEIIKPQRRKYFSSTMKNVT-----
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Heard J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 AA;
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                                                                                                                                                                               entry)
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Pred. No. 1e-43;
6; Mismatches
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                                                                                         senescence.
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22-AUG-2001; 28-FEB-2002

2001WO-US26189

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                                                                                                                                                                                                 are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a common composition of the polynucleotides are computed in the polynucleotide is sequence information selected from plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a composition of the polynucleotide or antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified production of agriculturally useful proteins or metabolic chemicals, pest tolerance, herbicide resistance, seed and fruit yield, growth disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 proteins which are
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95%
                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An isolated or recombinant polynucleotide used to produce a transgenic
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KEDDIE J.
ADAM L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK65363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M, Creelman
Ratcliff O,
                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PINEDA O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIECHMANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREELMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MENDEL BIOTECHNOLOGY INC
GKLCSDEVDLVLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHDERCCKTKMI-
                                                      GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLN----TTKIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 880-881; 941pp;
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                                                                                                                                                                            246
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2000US-0713994.
2001US-0837944.
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                                                                                                                               36.7%;
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                                                                                                                  26;
                                                                                                                               Score 542.5; DB
Pred. No. 1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                  Mismatches
                                                                                                                                             DB 23;
                                                                                                                  52;
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L, Yu G;
                                                                                                                 Indels
                                                                                                                                             Length
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Pineda O;
                                                                                                                                              246;
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                                                                                                               Gaps
                          122
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ARUSULT 4
ARUST734
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                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAF or PAP2. The genes for both PAP1 and PAP2 have been mapped to chromoso 1. PAP1 and PAP2 are MYB-like transcription factors that regulate the production of anthocyanin pigment. The nucleotide sequence of the invention is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The nucleotide sequence is also useful for screening for PAP gene expression. At thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour expression. The nucleotide sequence is also useful for enhancing accumulation of phenylpropanoid product in a plant. A transgenic plant is useful for detecting a stress condition such as light appears a stress that it is useful for enhancing than the plant is useful for enhancing accumulation of phenylpropanoid product in a plant. A transgenic plant is useful for detecting a stress condition such as light appears to the product of the plant of t
                                                                                                                                                                                                                                                        stress, water stress, pH stress, temperature stress, heavy metal stress, pathogen attack or infection, wounding, nutrient deficiency, herbivory, or abnormal hormone levels in a plant. PAP1 or PAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated PAP1 or PAP2 gene, useful for increasing pigmentation in plants, as reporter genes for analysing expression pattern of promoter of interest, and to increase flux through phenylpropanoid pathway
                                          plants to respond more quickly to a stress condition in ways that are physiologically significant, as well as in ways of ornamental
                                                                                             colouration in ornamental plants for commercial sates, and to screes. Introduction of PAP1 or PAP2 sensitises sensitising plants to stress. Introduction of PAP1 or paper sensitises
                                                                                                                                                                        overexpression can also be useful in developing or enhancing d colouration in ornamental plants for commercial sales, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to the nucleotide and protein sequences of novel Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 26-27; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borevitz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-2000; 2000US-0603244.
05-JUL-2000; 2000US-0610185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SALK )
(ROBE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sensitisation; chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SALK INST BIOLOGICAL STUDIES.
ROBERTS NOBLE FOUND INC SAMMUEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNKDEOKDKLININLLDGDNMWWESLLE 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REKINNKCGEISTKIEIIKPORRKYFSSTMKNVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wounding; nutrient deficiency; herbivory; plant colouration;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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sequence

the A. thaliana PAP1

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ARBSULT 5
AAB68356
AC AAB6
XX MYB
DT 09-J
XX Stre
XW MYB
PN WO20
XX O6-N
XX O6-N
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Best Local
            The present sequence represents a plant stress tolerance-related myloblastosis (MYB) transcription factor. The specification describes AtmYB60, AtmYB76, AtmYB75 and AtmYB90. MYB polypeptides are useful for enhancing a plant's tolerance or sensitivity to stress e.g. salt, drought, cold and heat tolerance. It is also useful for producing a
                                                                                                                        Nucleic acid molecules encoding plant stress tolerance-related myloblastosis transcription factors for increasing stress resing a crop in a field -
                                                                                                                                                                                WPI; 2001-316365/33.
N-PSDB; AAF85191.
                                                                                                                                                                                                                                                                              05-NOV-1999;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Stress tolerance; myloblastosis transcription factor; heat tolerance; MYB transcription factor; AtMYB60; AtMYB764; AtMYB75; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
 transgenic plant
                                                                                              Claim 13; Fig 4; 92pp; English
                                                                                                                                                                                                                                                                                                                        06-NOV-2000; 2000WO-US30503
                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis sp
                                                                                                                                                                                                                                                                                                                                                                                                                                  phenylpropanoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB68356 standard; Protein;
                                                                                                                                                                                                                          Tonelli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNL-----LRKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEISPPLNIGEGNSMQQGQISHENWGEFSLNLPPMQQGVQNDDFSAEID-LWNLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of MYB
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  enhanced stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription factor AtMYB90.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 538; DB 23;
Pred. No. 2.8e-43;
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    tolerance
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                                                                  PILGRIM M.
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify phrenyl lipid content, to modify fatty acid and modify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is Arabidopsis thaliana transcription factor The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g. potato and cotton plants, when their expression level is altered.
                                                                                                                                                                                                                                     Agriculture; metal microbial disease
                                                                                                                                                                                                                                                                                                                       Arabidopsis transcription
                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU92969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU92969 standard; Protein; 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                             WO200215675-A1
                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                           plant; transcription factor; transgenic.
                                                                                                                                                                                                      fruit yield; growth rate; leaf senescence; flower senescence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
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                                                                                                                                                                                                                               metabolic chemical; environmental stress; sease resistance; herbicide resistance; se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potential in agricultural biotechnology for modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVCENSITCNKDDEKDDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.1%; Score 532.5; DB 22;
44.4%; Pred. No. 9.7e-43;
Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133pp; English.
                                                                                                                                                                                                                                                                                                                       factor #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                     ss; drought;
seed yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNLMNGDNMWLENLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g., corn
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64

GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126

GRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHESSCCKSKMKK

123

SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR

SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR

63 66

4 7 Matches 122; Query Match Best Local 9 Sequence

Similarity

36.1%;

Conservative

34; Score Pred.

Mismatches 532.5; DB 2 No. 9.7e-43;

76;

Indels Length 249;

43;

Gaps

DB 23;

249

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cc complements, fragments, or related polynucleotide with 31% to 95% cc sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant trait as compared cc phenotype as compared to a wild-type or reference plant, or the plant or the plant or the plant can altered trait as compared to a wild-type or reference plant, or the plant or the plant cc are a transgenic plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer comprising inputting sequence information, and identifying a comprising inputting sequence information, and identifying a comprising inputting sequence information. The isolated or recombinant polynucleotide is used for producing a plant having a comprising a polynucleotide trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polynucleotide or polynucleotide or antisense nucleic acid into an expression vector, into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified comprising for a modified trait (e.g. increased plant, microbial comprising as response (e.g. drought), microbial codisease resistance, herbicide constitutions (e.g. drought), microbial
pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 40; Page 97-98; 941pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated or recombinant polynucleotide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-2000;
16-NOV-2000;
                                               specification).
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ADAM/)
(RATC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEND-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PINE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KEDD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-292022/33.
                            leaf and flower senescence and many other traits listed fication). The present sequence is one of the 232 proteir aliana transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           m M, CIC.
, Ratcliff (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEARD J.
JIANG C.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK65155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REUBER J L.
RIECHMANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADAM L.
RATCLIFF O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Creelman latcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-227439P.
; 2000US-0713994.
; 2001US-0837944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reuber JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dubell AJ, Heard J,
uber JL, Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang C,
L, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            produce a transgenic
                                               proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pineda 0;
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RESULT 8
ARBSOLT 8
ARBSOLT 8
ARBSOLT 8
ID ARBSOLT 8
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                                                                                          a Mentha sp. or Taxus sp. terpenoid pathway gene where the terpenoid pathway gene encodes limonene synthase (LS) or taxadiene synthase (TDS). It is also useful for identifying one or more transcription factors that activate one or more genes of a biological pathway of a plant, fungi or animal cell, where the biological pathway can be a biochemical pathway such as biosynthetic pathways for soluble and insoluble carbohydrates, for amino acids and a response pathway to abiotic stress such as cold, freezing, drought, heat, nutrient deficiency, pH or biotic stress such as singal, viral or bacterial infection, developmental pathway such as fingal, viral or bacterial infection, developmental pathway such as
                                                                                                                                                                                                                                                                                                                                                                                                                    a polynucleotide which encodes a transcription factor for controlling the expression of one or more genes in a pathway. The method is useful for determining whether a member of a pool of test transcription factor polynucleotides encodes a biosynthetic pathway transcription factor or a primary metabolite pathway gene or a secondary metabolite pathway gene such as a terpenoid or alkaloid pathway gene transcription factor. It is also useful for determining whether a member of a pool of test encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription factor; metabolite pathway; terpenoid; limonene synthase; alkaloid pathway gene; taxadiene synthase; biological pathway; freezing; abiotic stress; cold; drought; heat; nutrient deficiency; biotic stress; infection; developmental pathway; flowering; root development; TDS; LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining whether one of several test transcription factor (TF) polynucleotides encodes pathway TF by determining expression from pathway gene promoter linked to reporter gene in a cell in present
                                    flowering, roc
such as light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-018799/01.
N-PSDB; AAD47497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana G663 transcription factor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2002; 2002WO-US07999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVDPWWINLLEN----CNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNIISPPTTPVQKIGVFKPRPRSF---SVNNGCSHLNGLPEVDLIPSCLGLKKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNKCGEIST---KIEIIKPQRRKYFSSTMKNVTNNNVILDEEBHCKEIISEKQTPDASMD
                                    root development, a response pathway to environmental cues ght intensity and light quality, circadian rhythm. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates to a high-throughput method for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221pp; English.
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                                       Sequences
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Best Local S
Matches 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAP2; production of anthocyanin pigment; MYB-like transcription transgenic; plant; phenylpropanoid; stress; light stress; water pH stress; temperature stress; heavy metal stress; pathogen atta pH stress; wounding; nutrient deficiency; herbivory; plant colou
                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                       misc_difference
                                                                                                                                                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                                   misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. thaliana Production of anthocyanin pigment 2 (PAP2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU75735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU75735 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is Arabidopsis thaliana G663 transcription factor protein.
               Borevitz J,
                                                                                          23-JUN-2000; 2000US-0603244.
05-JUL-2000; 2000US-0610185.
                                                                                                                                      21-JUN-2001; 2001WO-US19734.
                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                              (SALK )
(ROBE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 sensitisation; chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                            SALK INST BIOLOGICAL
                                               ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLGVRKGSWTDEEDFILRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GÉN-QEADAIVPEATTAEHGATLAFDVEQLWSLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HENWGEFSLILPPMQQGVQNDDFSAEID-LWNLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVDPWWINLLEN---CNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQQQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNIISPPTTPVQKIGVFKPRPRSF---SVNNGCSHLNGLPEVDLIPSCLGLKKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNKCGEIST---KIEIIKPORRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRLSNDEVDILLRIHKLIGNRWSLIAGRIPGRTANDVKNYWNTHISKKHESSCCKSKMKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249
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                 Xia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---NVCENSITCNKDDEKDDFV--
                                                                                                                                                                                                                                                                            /note=
215
                                               NOBLE
                                                                                                                                                                                                                                                                                                                                           161
                                                                                                                                                                                                                                                                                                           190
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                  /note= "Encoded by
                 ×
                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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                 Lamb
                                               FOUND
                                                                                                                                                                                                                                                             "Encoded by
                                                                                                                                                                                                                                                                                          "Encoded by
                                                                                                                                                                                                                                                                                                                          "Encoded by GAA"
                                                                                                                                                                                                                                                                                                                                                        "Encoded by
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                                               INC
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Pred.
                                                             STUDIES
                 Dixon RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                               SAMMUEL
                                                                                                                                                                                                                                                             · GAT"
                                                                                                                                                                                                                                                                                            GAT"
                                                                                                                                                                                                                                  GAG
                                                                                                                                                                                                                                                                                                                                                        CCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532.5; DB 2
No. 9.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant colouration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NNLMNGDNMWLENLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               water stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor;
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208 240 174 183 126 63 66 7;

2002-164443/21.

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ARBSULT 10
AAU93155
ID AAU9315
AC AAU93
XX AAU93
XX Arabi
XX Arabi
XX Agric
KW Agric
KW Fruit
KW Fruit
KW Fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    production of anthocyanin pigment. The nucleotide sequence of the circumstance is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The nucleotide sequence is also useful for screening for plant cell (e.g., A. thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour expression. The nucleotide sequence is also useful for enhancing caccumulation of phenylpropanoid product in a plant. A transgenic plant is useful for detecting a stress condition such as light carest, water stress, pH stress, temperature stress, heavy metal stress, pathogen attack or infection, wounding, nutrient deficiency, therefore, pathogen and bormone levels in a plant. PAP1 or PAP2 colouration in ornamental plants for commercial sales, and for colouration plants to stress. Introduction of PAP1 or PAP2 sensitises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants to respond more quickly to a stress condition in ways that physiologically significant, as well as in ways of ornamental significance. The present sequence represents the A. thaliana PAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated PAP1 or PAP2 gene, useful for increasing pigmentation in plants, as reporter genes for analysing expression pattern of promoter of interest, and to increase flux through phenylpropanoid pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABK14222
                                                        plant; transcription
                                                                         microbial disease resistance; herbicide resistance; fruit yield; growth rate; leaf senescence; flower so
                                                                                                                                                          Arabidopsis transcription factor #193.
                                                                                                                                                                                                    02-JUL-2002
                                                                                                                                                                                                                                                                               AAU93155 standard; Protein; 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein sequence of the invention.
                  Arabidopsis thaliana
                                                                                                                  Agriculture; metabolic chemical; environmental stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAP1 and PAP2 are MYB-like transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to the nucleotide and protein sequences of novel idopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 AP2. The genes for both PAP1 and PAP2 have been mapped to chromosome
                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
                                                                                                                                                                                                                                                                                                                                                                                                                     163 DEEEHCKEIISEKOTPDASMDNVDPWWINLLENCNDDIEEDEEVV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Page 28; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                 NKDDEKXDFVN-----NLMNGDNMW---LENLLGENQEAXAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNIISPSTTPVQKIGVFKPRPRSFSVNNGCSHLNGLPXVDLIPSCLGLKKNNVCENSITC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNKCGEIST---KIEIIKPQRRKY--------FSSTMKNVTNNNVIL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHESSCCKSKMKK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.7%;
                                                          factor; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 527; DB 23;
Pred. No. 3.3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                             senescence.
                                                                                                                  drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
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SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR

SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR

GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK---

114 63 66 5

Query Match Best Local : Matches

Similarity

35.5%;

Score 524; DB 2 Pred. No. 5e-42; Mismatches

DB 23; Length 212;

102; 7

Conservative

33;

38;

Indels

38;

Gaps

Sequence

212

A

S

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CC associated with a plant trait as compared to a wild plant. Also included CC are a transgenic plant comprising the polynucleotides, a computer CC readable medium having stored sequence information, and identifying a CC homologue sequence from a database comprising a plurality of known plant CC 464 fully defined sequences given in the specification. The isolated or CC recombinant polynucleotide is used for producing a plant having a CC modified trait, the method comprising selecting a polynucleotide that CC encodes a polypeptide or an antisense nucleic acid, inserting the CC polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress CC introducing the vector into a plant or a cell of a plant to overexpress CC plant, and selecting for a modified trait (e.g. increased CC plant, and selecting for a modified trait (e.g. increased CC plant, and selecting for a modified trait (e.g. increased CC plant, and selecting for a modified trait (e.g. drought), microbial CC disease resistance, herbicide resistance, seed and fruit yield, growth C ate, leaf and flower senescence and many other traits listed in the CC pecification). The present sequence is one of the 232 proteins which are CC A. thaliana transcription factors.
                                                                                                                                                                                                                                                                                                                                                                           encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated or recombinant polynucleotide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pilgrim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-2000; 2000US-227439P
16-NOV-2000; 2000US-0713994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200215675-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DUBE/)
(HEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEND-)
(PILG/)
(CREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-2001; 2001US-0837944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RATC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADAM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KEDD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-292022/33.
DB; ABK65341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Page 794-795; 941pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEARD J.
JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATCLIFF O. REUBER J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M, Creelman
Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PINEDA O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIECHMANN J
YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILGRIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiang
,, Yu G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  produce a transgenic
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                                                  proteins which are
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209; 79;

Gaps

126

63

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ARESULT 11
ARABOL 1933
ID AREOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-1999;
17-APR-2000;
22-AUG-2000;
The present sequence is homologue G2421 of Arabidopsis thaliana transcription factor G663. The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify the insoluble sugar content of seeds, to modify the oil content of seeds also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reuber
Pineda
                                                                                                                                                                                                                                                                                          Nucleic acids encoding plant transcription factor polypeptides, useful for altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structural characteristic; agricultural biotechnology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-NOV-2000; 2000WO-US31457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription factor; trait modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2001
                                                                                                                                                                                                                                           Claim 4; Page 116; 133pp; English
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(REUB/)
(CREE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RIEC/
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DB; AAD05768.
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YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILGRIM M.
RIECHMANN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREELMAN
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Heard J;
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2000US-0197899.
2000US-0227439.
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Best Local S
Matches 120
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                                                                                                   (MEND-)
(PILG/)
(CREE/)
(DUBE/)
(HEAR/)
(JIAN/)
(KEDD/)
(ADAM/)
(RATC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agriculture; metabolic chemical; environmental stress; microbial disease resistance; herbicide resistance; see fruit yield; growth rate; leaf senscence; flower senscenter; transcence; flower senscenter; flower
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16-NOV-2000; 2000US-0713994
16-APR-2001; 2001US-0837944
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       (RIEC/)
(YUGG/)
(PINE/)
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                                                                            (REUB/)
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120; Conserv
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                                                                                                                                                                        CREELMAN R.
DUBELL A J.
HEARD J.
JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                           KEDDIE J.
ADAM L.
                                                                            RATCLIFF O. REUBER J L.
                                                                                                                                                                                                                                                                                               MENDEL BIOTECHNOLOGY
       PINEDA
                                RIECHMANN
YU G.
                                                                                                                                                                                                                                                                         PILGRIM M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEPCCKTKIKRINIITPP----NTPAQKVCENSITCNKDD-----
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No. 1.7e-41;
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RESULT 13
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AC AAB68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are a transgenic plant comprising the polynucleotides, a computer creadable medium having stored sequence information, and identifying a computer compose sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 46 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that composes a polypeptide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid, inserting the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased plant, and selecting for a modified trait (e.g. increased plant, and selecting for a modified trait (e.g. drought), microbial composition of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial constituence, herbicide resistance, seed and fruit yield, growth rate, leaf and flower sensescence and many other traits listed in the specification. The present sequence is one of the 232 proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one-or more genes associated with a plant trait as compared to a wild plant. Also included
09-JUL-2001
                                       AAB68355;
                                                                          AAB68355 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated or recombinant polynucleotide used to produce
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DB; ABK65362.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   GKFSSDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKK-------
                                                                                                                                                                                                                 ENWGEFSLNLPPMQQGVQNDDFSAEIDLWNLLD
                                                                                                                                                                                                                                                      MVGDNIWLERL-----LDEGQEVDVLVTEAAATE--
                                                                                                                                                                                                                                                                                           --- DPWWINLLENCNDDIEEDEEV-VINYEKTLTSLLHEEISPPLNIGEGNSMQQGQISH
                                                                                                                                                                                                                                                                                                                                    HEPCCKTKIKRINIITPP----NTPAQKVCENSITCNKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                           GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKGLRXGAWTAEEDSLLRQCIGKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR

    Creelman
Ratcliff O,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.1%; Score 518.5; DB 23;
44.0%; Pred. No. 1.7e-41;
tive 29; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dubell AJ, Heard J, uber JL, Riechmann JL,
                                                                            211 AA
                                                                                                                                                                          -FDVE-QLWNLFD 202
                                                                                                                                                                                                                 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jiang C,
L, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                    ----EK---DDFVDNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  listed in the proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Keddie J;
Pineda O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209;
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                                                                                                                                                                                                                                                        KEGTLA-
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                                                                                                                                                                                                                                                                                                                                    156
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                                                                                                                                                                                   Query Match
Best Local S
Matches 103
                                                                                                                                                                                                                                                                           The present sequence represents a plant stress tolerance-related myloblastosis (MYB) transcription factor. The specification describes AtMYB60, AtMYB764, AtMYB75 and AtMYB90. MYB polypeptides are useful for enhancing a plant's tolerance or sensitivity to stress e.g. 'Salt, drought, cold and heat tolerance. It is also useful for producing a transgenic plant with enhanced stress tolerance or stress sensitivity. MYB polypeptides are also useful for increasing the production of products of the phenylpropanoid biosynthesis pathway, e.g. stilbenes, flivenoids, lignins, salicylic acid, anthocyanins, and phenolic
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding plant stress tolerance-related myloblastosis transcription factors for increasing stress resistance of a crop in a field -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                    derivatives.
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Fig 3B; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-1999;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2000; 2000WO-US30503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-316365/33.
                         124 DITPIPTTPALKNNVYKPRPRSFTVNNDCNHLNAPPKVDVNPP----CLGLNINNVCDNS
160 VILDEEEHCKEIISEKQTPDASMDNVDPW 188
                                                                            64
                                                                                                        67
                                                                                                                                                                                     103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid sequence
                                                                                                                                 4
                                                                                                                                                                                   Similarity. 49.:
03; Conservative
                                                                             GKLSSDEVDLLLRLHRLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKIKMKKR
                                                                                             GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK-------
                                                                                                                                SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                              SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                                                                                                                                                                        211
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2000US-0693855.
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173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myloblastosis transcription factor; factor; AtMYB60; AtMYB764; AtMYB75;
                                                  LNTTKIVPREK---INNKCGEIST--KIEIIKPQRRKYFSSTMKNVTNNN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of MYB transcription factor AtMYB75
                                                                                                                                                                                  34.5%; Score 510; DB 22;
49.3%; Pred. No. 1.1e-40;
tive 25; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Tyr encoded by ATATAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCGAT"
                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                           Length 211;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heat tolerance;
transgenic plan
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                                                                                                                                                                                   Gaps
                         179
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ARBSULT 14
ARAB2483
IID 8AB88
XX AAB8
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XX GOSS
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XX W11-D
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PF 01-D
XX WPI;
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Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor GhAYB 7. The sequence was deduced from GhAYB 7 cDNA isolated from a Gossypium hirsutum cv. Acala SJ-2 10-day pre-anthesis fibre cDNA library. A claimed method of modulating transcription in a plant involves introducing into the plant a recombinant expression cassette comprising a promoter that is operably linked to a heterologous polymucleotide encoding a MYB protein, especially GhMYB 1 or GhMYB 6. The plant is especially a cotton plant, and the promoter directs expression of the polymucleotide in cotton fibres or roots. Valuable phenotypes can be conferred on the plant by this method, e.g. increased fibre quality, yield, length, strength or fineness, alteration of root architecture, and enhanced growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulating transcription in plants for improving cotton fiber quality comprises introducing a recombinant expression cassette comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cotton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of cotton R2R3-MYB transcription factor GhMYB 7. The sequence was deduced from GhMYB 7 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 23; Page 44; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter operably linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF90596.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GhMYB 7; MYB; cotton; transcription factor; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                        AAPSKN------
                                                                                                                                                                                                                                            HIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVP 122
                                                                                                                                                                                                           DIKRGNISPDEEELIIKLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTNLSKRVSDRQKSP
QTPDASMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQ 235
                                                                                                                                                                                                                                                                                                                        SPCCSKEGLNRGAWTALEDKILKDYIKVHGEGRWRNLPKRAGLKRCGKSCRLRWLNYLRP
                                                                                                                                                                                                                                                                                                                                                                      STSMSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRP
                                                                                                                                           REKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNN-----NVILDEEEHCKEIISEK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302
                                                                                                                                                                                                                                                                                                                                                                                                                                         28.6%;
larity 37.3%;
Conservative :
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                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 422; DB 22; pred. No. 5.3e-32; 34; Mismatches 96
                                                                                        PEAARRGTAGNGNTNGNGSGSSSTHVVRTRATRCSKVFI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
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                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a plant having cacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; homeodomain zipper; LIM domain; AP2; EREB8; zinc finger domain; type 2 CysHis2: CCAAT box element. MYD
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1999;
18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Pages 716-717; 747pp; English
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FLETCHER CHALLENGE FORESTS LTD.
                                 FEQDEVDLILRLHKLLGNRWSLIAGRLFGRTANDVKNYWNTNLLRKLNTTKIVFR-----
                                                                                                                                               LGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGD
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ILPEEEDLILRLHRLLGNRWSLIAGRMPGRTDNEVKNYWNTHLSKKLISQGIDPRTHKPL
                                                                                                                VGLNRGPWTPEEDLCLSNYIEAHGEGGWRTLPKKAGLLRCGKSCRLRWMYLRPDVKHGH
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                                                                                                                                                                                                                              Score 420; DB 21;
Pred. No. 1.2e-31;
5; Mismatches 91;
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Search	рь	8	Db	Ş	В	8	
Search completed: January 29, 2004, 20:11:24	237 HNKGSKQVPEPLSNTACENSSAQGVAGD 264	230 EGNSMQQGQISHENWGEFSLNLPPMQQGVQND 261	183 LPENQLLETSNSQCPSVATDFVPQAPSIPSTAYSFQQSTTSSVPGGVSDSVDVN 236	181 SMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIG 229	130 SESEDICSSPGNSEVSRKSQRENNAEIPRKVADGAVDIQDKEEDITEDQTSAQ 182	124EKINNKCGEISTKIEIIKPORRKYFSSTWKNVTNNNVILDEEEHCKEIISEKOTPDA 180	

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Title:
Perfect score:
Sequence:
                                                                                                                                                  Database :
                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
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Gapop 10.0 , Gapext 0.5
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1477
1 MNSTSMSSLGVRKGSWTDEE.....QQGVQNDDFSAEIDLMNLLD 274
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	0	ហ	4	w	2	1	No.	Result	
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8.6	•			8.9	•	9.1	9.1		9.3		9.3	9.3	•	9.3	10.7	16.0	16.0	16.3	16.3	16.4	16.4	:	21.5	٠	35.7	6		Query	æ
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US-09-610-185C-4

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RESULT 3
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Best Local Similarity 48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/610,185C CURRENT FILING DATE: 2000-07-05 PRIOR APPLICATION NUMBER: US 09/603,244 PRIOR FILING DATE: 2000-06-23 NUMBER OF SEQ ID NOS: 11 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Borevitz, Justin APPLICANT: Xia, Yiji
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dixon, Richard A.
APPLICANT: Lamb, Christopher J.
APPLICANT: Lamb, Christopher J.
TITLE OF INVENTION: REGULATION OF
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: SALKINS.003C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(249)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
SOFTWARE: PastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/08/722,
FILING DATE: 27-SEP-1996
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yang, Yinong
APPLICANT: Klessig, Daniel, F.
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                              STREET: 1001
                                                                                                        COMPUTER:
                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 DEEEHCKEIISEKQTPDASMDNVDPWWINLLENCNDDIEEDEEVV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 KNIISPSTTPVOKIGVFKPRPRSFSVNNGCSHLNGLPXVDLIPSCLGLKKNNVCENSITC 183
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                                                                                                                                                                                            USA
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                                                                                                        IBM Compatible
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                    US/08/722,626B
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Pred. No. 3.1e-47;
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                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08997251 Patent No. 6271440
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                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GUBLER, FRANZ J.
APPLICANT: JACOBSEN, JOHN V.
TITLE OF INVENTION: PLANT REGULATORY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: 1
ANTI-SENSE: NO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                      STREET:
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APPLICATION NUMBER:
                                                                                                                     COUNTRY: U
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REGISTRATION NUMBER: 27,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEFAX: 215 563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                    222 STDHVMVAANQELQVQLPFSSFKEENVDILATKMEDDMDFW 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 MGLKKGPWIPEEDQILISFIQTNGHGNWRALPKQAGLLRCGKSCRLRWTNYLRPDIKRGN
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                                                                                                                                                                       Boulder
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5370 Manhattan Boulevard
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US/08/997,251
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Pred. No. 9.8e-31;
                                  Version
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23-DEC-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Winner, Ellen P.
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN3779/95
FILING DATE: 23-JUN-1995
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GUBLER, FRANZ J.
APPLICANT: JACOBSEN, JOHN V.
TITLE OF INVENTION: PLANT REGULATORY PROTEINS III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1'CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                STREET: 50 
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CLASSIFICATION:
                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 PPMQQGVQNDDFSAEIDLW 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 VVINYEKTLTSL----LHEEISPPLNIGEGNSMQQGQISHENWGEFS------LNL 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 SNEDQQGSSDFNCGE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 QDEVDLILRLHKLIGNRWSLIAGRIPGRTANDVKNYWNTNILR-KLNTTKIVPREKINN- 128
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                                                                                                                                                                                                                                                                      5370 Manhattan Boulevard
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                                                                                                                                                                                                                                                                                                              Greenlee, Winner and Sullivan, P.C.
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Best Local Similarity
Matches 65; Conserva
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                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                           Patent No. 6410825
                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Temple University - Of The Commonwealth System of APPLICANT: Toscani, Antonio
APPLICANT: Hatton, Kimi
APPLICANT: Reddy, E. P.
TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: AU PI
FILING DATE: 23-UUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO AU96/00383 FILING DATE: 21-JUN-1996 PRIOR APPLICATION DATA:
  COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                   STATE:
                                                                                                ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C. STREET: Suite 1800 Two Penn Center Plaza CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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REGISTRATION NUMBER: :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 VRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFE 70
                                                                               PA
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Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---YPTSVCNQSSNEDQQCSSDFDCGENLSNDLLNANGLYLPDFTCD 194
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                                                                                                                                                                                                                                                                                                      Of The Commonwealth System of Higher Education
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IBM PC compatible YSTEM: PC-DOS/MS-DOS

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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
                                                       ATTORNEY/AGENT INFORMATION:
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-8383
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                                                                                                                                                                                                                                                                                                                                                                 STREET: SEIDEL, GONDA, LAVORGNA & MONACO, P.C. CITY: Philadelphia
STATE: Pa
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60
                                                                                  FILING DATE:
                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          ZIP: 19102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 16.4%; Score 242.5; DB 4; scoral Similarity 43.7%; Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 EDRIIYEAHKRLGNRWAEIAKLLPGRTDNSIKNHWNSTMRRKV 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGPWTKEEDQRVIELVQKYGPKRWSLI-AKHLKGRIGKQCRERWHNHLNPEVKKSSWTEE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               751 amino acids
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Hatton, Kimi
Reddy, E. P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Temple University - Of The Commonwealth System of Higher Education
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      6056-214 PC
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US-08-928-941D-4
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GENERAL INFORMATION:
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Best Local Similarity 43.7%; Pred. No. 1.1e-16
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                                                                                                                                                                                              TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO:
                               MOLECULE TYPE: I
HYPOTHETICAL: NO
FRAGMENT TYPE: I
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CIP
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                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/928,941D FILING DATE:
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                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                  ORGANISM:
                                                                                                        TOPOLOGY:
                                                                                                                     STRANDEDNESS:
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                                                                                                                                          amino acid
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                  Mus musculus
                                                                   : protein
                                                                                                        linear
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Query Match Best Local Similarity

16.3%; 43.7%;

Score 240.5; DB 3; Pred. No. 1.9e-17;

Length 156;

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                                                                                                       Matches. 45;
                                                                                                                                    Query Match
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                                                                                                                      Local
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
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ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                          FRAGMENT TYPE:
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                                                                    13 KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 EVDLILRLHKLIGNRWSLIAGRIPGRTANDVKNYWNTNLLRKL 115
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   73 EVDLILRLHKLIGNRWSLIAGRIPGRTANDVKNYWNTNLLRKL 115
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/280,590A FILING DATE: 29-Mar-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                    KGPWTKEEDQRVIKLVQKYGPKRWSVI-AKHLKGRIGKQCRERWHNHLNPEVKKTSWTEE
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Inoue, Kazushi
                                                                                                                                                                                                                                        internal
                                                                                                                     16.3%; Score 240.5; DB 4
43.7%; Pred. No. 1.9e-17;
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                                                                                                       Mismatches
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Continental Plaza,
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                                                                                                                                    DB 4;
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                                                                                                                                    Length 156;
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                                                                                                                   US-09-280-590A-46
                                                                                                                                      RESULT 11
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                                                                  Sequence 46, Applicati
Patent No. 6303772
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Gal
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,941D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hirai,
APPLICANT: Sherr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hackensack Ave, Continental Plaza, STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
NUMBER OF SEQUENCES:
                                                                                                                         APPLICANT: Hirai, Hiroshi
                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                               114 EDRIIYQAHKRLGNRWAEIAKLLPGRTDNAIKNHWNSTMRRKV 156
                                                                                                                                                                                                                                                                                                                                                                                    55 KGPWTKEEDQRVIELVQKYGPKRWSVI-AKHLKGRIGKQCRERWHNHLNPEVKKTSWTEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                         13 KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD 72
                                                                                                                                                                                                                                                                                                                                       73 EVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKL 115
                                                                                                                                                                                       Application US/09280590A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08928941D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sherr, Charles
IVENTION: CYCLIN-D BINDING FACTOR, AND USES
IVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
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                                                              Sherr, Charles
Inoue, Kazushi
Bodner, Sarah M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.0%; Score 236.5; DB 3
42.7%; Pred. No. 4.9e-17;
rative 21; Mismatches 37
                   CYCLIN-D BINDING FACTOR, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
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ORGANISM: Gallus gallus sequence DESCRIPTION: SEQ ID NO: 46: US-09-280-590A-46
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-156-316-1
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US-09-156-316-1
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                                                                SEQ ID NO 1
LENGTH: 802
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            sequence 1, Application US/09156316
Patent No. 6183961
                                                                                                                                                     APPLICANT: Bernstein, Harold S.
APPLICANT: Coughlin, Shaun R.
TITLE OF INVENTION: Methods and Compositions for Regulating Cell Cycle
TITLE OF INVENTION: Progression
FILE REFERENCE: UCSF-020/01US
CURRENT APPLICATION NUMBER: US/09/156,316
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 60/060,688
EARLIER FILING DATE: 1997-09-22
                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,590A
FILLING DATE: 29-Mar-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 EDRIIYQAHKRLGNRWAEIAKLLPGRTDNAIKNHWNSTMRRKV 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGPWTKEEDQRVIELVQKYGPKRWSVI-AKHLKGRIGKQCRERWHNHLNPEVKKTSWTEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD 72
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STATE: New Jersey
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TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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42.7%;
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Sequence 17, Application US/08519103 Patent No. 5733730 GENERAL INFORMATION:

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; MOLECULE TYPE: peptide US-08-519-103-16
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RESULT 14
US-08-519-103-17
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                                                                                                                                 Matches
                                                                                                                                           Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CZANE-FEUTY, Sharon E.
REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0: FILING DATE: 25-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 TKIVPREKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 IKKTEWSREEEEKLLHLAKLMPTQWRTIA-PIIGRTAAQCLEHYEF-LLDKAAQRDNEEE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 IKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKL-----NT 117
                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 MSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGL--NRCRKSCRLRWLNYLRPH
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                                                                   1 VKKSSWTEEEDRIIYEAHKRLGNRWAEIAKLLPGRTDNSIKNHWNSTMRRK 51
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                             single
                                                                                                                                             9.3%;
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29.4%; Pred. No. 1e-
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                                                                                                                                11; Mismatches
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                                                                                                                                 Score 138; DB 1; 1
Pred. No. 2.1e-07;
1; Mismatches 16;
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                                                                                                                                                              Length 51;
                                                                                                                                 Indels
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                               APPLICANT: Broccoli, Dominique
APPLICANT: Smogorzewska, Agata
TITLE OF INVENTION: TELLOMERE REPEAT BINDING FACTOR AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER
                                     ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                    STREET: 41.
STREET: Hackensack
CITY: Hackensack
STATE: New Jersey
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STREET: 411
STREET: Hackensack
CITY: Hackensack
CTATE: New Jersey
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E.
REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: KLAUBER & JACKSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 25-AU
CLASSIFICATION:
                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.3%; Score 138; DB 1;
49.0%; Pred. No. 2.1e-07;
ative 11; Mismatches 15
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TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                            US/09/018,635
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Search completed: January 29, 2004, 20:13:54 Job time : 22 secs
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: David A. Jackson
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                24;
                                                                                                             64 IKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK 114
                                                                           1 VKKSSWTEEEDRIIYEAHKRIGNRWAEIAKLIPGRTDNSIKNHWNSTMRRK 51
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Pred. No. 2.1e-07;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model ~

Run on: January 29, 2004, 20:12:52; Search time 33 Seconds (without alignments)
1725:570 Million cell updates/sec

Title: US-10-033-190-2
Perfect score: 1477
Sequence: 1477
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580
Minimum DB seq length: 0
Minimum DB seq length: 2000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/US09E\_PUBCOMB.pep:\*
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
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17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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394	396.5	396.5	397	401	401	408	408	423.5	518.5	524	532.5	532.5	542.5	1477	Score		
26.7	26.8	26.8	26.9	27.1	27.1	27.6	27.6	28.7	35.1	35.5	36.1	36.1	36.7	100.0	Match Length DB	Query	ф
363	302	302	342	203	203	269	269	249	209	212	249	249	246	274	ength l		
12	14	9	11	12	11	15	11	15	11	11	15	11	11	14	BB		
US-10-093-837-2	US-10-008-118A-12	US-09-443-704-12	US-09-934-455-252	US-10-407-920-29	US-09-934-455-390	US-10-278-173-72	US-09-533-029-94	US-10-286-264-148	US-09-934-455-480	US-09-934-455-438	US-10-295-403-44	US-09-934-455-14	US-09-934-455-482	US-10-033-190-2	ID		
Sequence 2, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 252, App	Sequence 29, Appl	Sequence 390, App	Sequence 72, Appl	Sequence 94, Appl	Sequence 148, App	Sequence 480, App	Sequence 438, App	Sequence 44, Appl	Sequence 14, Appl	Sequence 482, App	Sequence 2, Appli	Description		1**

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
368	368	368	368.5	370	370	370	371	373	373	373.5	373.5	374	374	374	374	374	377	377	377	377	377.5	379.5	379.5	385	385	387.5	387.5	393	393
	24.9	24.9	24.9	25.1	25.1	25.1		25.3		25.3			25.3	25.3	25.3	25.3	25.5					25.7					26.2	26.6	26.6
305	120	120	333	245	149	149	332	282	281	335	295	371	371	371	273	273	349	349	268	268	274	258	258	246	246	253	253	120	120
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US-09-443-704-8	US-10-008-118A-50	US-09-443-704-50	US-10-278-173-146	US-10-295-403-60	US-10-008-118A-30	US-09-443-704-30	US-10-021-811-54	US-10-225-068-10	-10 - 295	-10-295-	US-10-278-173-152	US-10-278-536-40	US-09-934-455-66	US-09-533-029-86	US-10-008-118A-20	US-09-443-704-20	US-10-278-536-114	US-10-278-173-138	US-10-008-118A-34	US-09-443-704-34	US-10-278-536-36	US-10-008-118A-4	US-09-443-704-4	US-10-008-118A-32	US-09-443-704-32	US-10-008-118A-28	US-09-443-704-28	US-10-008-118A-6	US-09-443-704-6
Sequence 8, Appli	(0	, ,	146,	60,		Sequence 30, Appl	54	10,	46,		152,	40,	66,	86,	e 20	õ,		138,	æ		36	о 4		N	32	e 28,	,	Sequence 6, Appli	Sequence 6, Appli

# ALIGNMENTS

RESULT 1 US-10-033-190-2

γQ	₽ <b>Q</b>	당 왕	유 성	Query Best Matcl	Sequence of Sequen
181 SMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQIS 240	121 VPREKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDA 180 	61 RPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLÞGRTANDVKNYWNTNLLRKLNTTKI 120 	1 MNSTSMSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYL 60	Query Match 100.0%; Score 1477; DB 14; Length 274; Best Local Similarity 100.0%; Pred. No. 2.3e-135; Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Publication US/10033190 Publication No. US20020133848A1 GENERAL INFORMATION: APPLICANT: Exelixis Plant Sciences, Inc. TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF AN ANTHOCYANIN MUTANT (ANTITILE OF INVENTION: TOMATO FILE REFERENCE: ED01-002C CURRENT APPLICATION NUMBER: US/10/033,190 CURRENT APPLICATION NUMBER: US/10/033,190 CURRENT FILING DATE: 2001-10-29 PRIOR APPLICATION NUMBER: US 60/244,685 PRIOR APPLICATION NUMBER: US 60/244,685 PRIOR FILING DATE: 2000-10-30 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PatentIn version 3.1 SEQ ID NO 2 LENGTH: 274 TYPE: PRT ORGANISM: Lycopersicon esculentum US-10-033-190-2

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; TYPE: PRT
; ORGANIEM: Arabidopsis thaliana
US-09-934-455-482
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CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
                                                                               Sequence 14, Application US/09934455 Publication No. US20030121070A1 GENERAL INFORMATION:
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                                          APPLICANT: Adam, APPLICANT: Cree
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APPLICANT: Cree
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TITLE OF INVENTION: Genes for Modifying Plant
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                                                                                                                                                                                                                                                               168 C-KEIISEKQTPDASMDNVDPWWINLLE 194
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Creelman, Robert
Dubell, Arnold
Heard, Jacqueline
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Heard, Jacqueline
Jiang, Cai-Zhong
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Ratcliffe, Oliver
Reuber, Lynne
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Yu, Guo-Liang
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b. US20030121070A1
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CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER FILING DATE: 2001-04-17
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 44, Application US/10295403 Publication No. US20030101481A1
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Best Local Similarity
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APPLICANT:
APPLICANT:
                  APPLICANT: Fromm, Mike
TITLE OF INVENTION: PLANT GENE SEQUENCES I
FILE REFERENCE: MBI-0003
CURRENT APPLICATION NUMBER: US/10/295,403
CURRENT FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-04-17 NUMBER OF SEQ ID NOS: 516
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                                                                                                                                                                                                                                                                                                        APPLICANT: Heard, APPLICANT: Riech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
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          PRIOR APPLICATION NUMBER: US/09/394,519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 NVDPWWINLLEN---CNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQIS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 HENWGEFSLNLPPMQQGVQNDDFSAEID-LWNLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122;
                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 KNIISPPTTPVQKIGVFKPRPRSF---SVNNGCSHLNGLPEVDLIPSCLGLKKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 NNKCGEIST---KIEIIKPORRKYFSSTMKOVTNNNVILDEEEHCKEIISEKOTPDASMD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
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Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
                                                                                                                      Keddie, James
Zhang, James
Benito, Maria-Ines
Yu, Guo-Liang
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                                                                                                                                                                                                  Pineda, Omaira
Reuber, Lynne
Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                 Broun, Pierre
                                                                                                                                                                                                                                                                                   Riechmann,
Adam, Luc
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Riechmann, Jose Luis
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                                                                                                                                                                                                                                                                                                                        Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.1%; Score 532.5; DB 1
44.4%; Pred. No. 1.6e-43;
tive 34; Mismatches 76
                                                                                                                                                                                                                                                                                                            Jose Luis
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Indels Length

43;

Gaps

63 66

242 274

208

174

PRIOR FILING DATE: 1999-09-13 PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 1998-09-22

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US-10-295-403-44
                PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
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LENGTH: 249
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Best Local Similarity 44.4%;
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APPLICANT:
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/934,455
                                                                                                                                                                                           APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
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SOFTWARE: PatentIn version 3.1
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APPLICATION NUMBER: 60/108,734
FILING DATE: 1998-11-17
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FILING DATE: 1998-09-22
APPLICATION NUMBER: 60/103,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 HENWGEFSLNLPPMQQGVQNDDFSAEID-LWNLLD 274
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Jiang, Cai-Zhong
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Riechmann, Jose Luis
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o. US20030121070A1
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PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF 'SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
SEQ ID NO 480
LENGTH: 209
TYPE: PRT
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LENGTH: 212
                                                                                                                                                   Matches
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Best Local Similarity
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                                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana -09-934-455-480
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for modifying Plant Traits IV
FILS REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22.
PRIOR APPLICATION NUMBER: 60/227439
PRIOR PILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
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                                                                                                                                                                     Local Similarity
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                                                                                                                                                   120;
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                                                                                                  7 SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGINRCRKSCRLRWLNYLRPHIKR
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                    GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126
                                                                        SSKGLRKGAWTAEEDSLLRQCIGKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
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Pilgrim, Marsha
Ratcliffe, Oliver
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Jiang, Cai-Zhong
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Riechmann, Jose Luis
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                                                                                                                                                     Conservative
                                                                                                                                                 35.1%; Score 518.5; DB 1
44.0%; Pred. No. 2.9e-42;
/ative 29; Mismatches 45
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                                                                                                                                                                                       DB 11; Length 209;
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CURRENT APPLICATION NUMBER: US/10/286,264
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 199-03-23.
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 148
LENGTH: 249
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G211
US-10-286-264-148
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APPLICANT: Riechmann, Jos
APPLICANT: Riechmann, Jos
APPLICANT: Zhang, James
APPLICANT: Zhang, Cai-Zho
APPLICANT: Pineda, Omaira
APPLICANT: Heard, Jacquel
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APPLICANT: Reuber, Lynne
APPLICANT: Pilgrim, Marsha
APPLICANT: Samaha, Raymond
TITLE OF INVENTION: POLYNUCLEOTIDES FOR SEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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221
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                                                                                                                      181 SMDNVDPWWINLLE------NCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNI 228
                                                                                                                                                                                                                                                                                                                                                                                                         cch 28.7%; Score 423.5; DB 15; Length 249;
al Similarity 36.5%; Pred. No. 6.5e-33;
100; Conservative 32; Mismatches 65; Indels 77;
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                                                                                                                                                                                                                                                                                                                           19 TKMGMKRGPWTVEEDEILVSFIKKEGEGRWRSLPKRAGLLRCGKSCRLRWWNYLRPSVKR 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNKCGEISTK-IEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMDNV 185
                                                                                                                                                                                                    NNKCGEISTKIEIIKPORRKYFSSTMKNVTNNNVILDEEE-----HCKEIISEKQTPDA 180
                                                                                                                                                                                                                                               GGITSDEEDLILRLHRLLGNRWSLIAGRIPGRTDNEIKNYWNTHLRKKLLRQGIDPQ--- 135
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                                                                                TVNGGDGDSKNSINVFGGEHGYEDFGFCYDD-----KFSSFLNSLIN-DVGDPFG- 220
                                                                                                                                                                                                                                                                  GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126
                                      GEGNSMQQGQISHENWGEFSLNLPPMQQGVQNDD
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Ratcliffe, Oliver
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Heard, Jacqueline
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                                                                                                                                                                -THKPLDANNIHKPEEEVSGGQKYPLEPISSSHTDDT 171
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                                        262
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APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
CURRENT FILING DATE: 1999-03-23
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 94
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US-10-278-173-72
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                                                                                                                                                                              Sequence 72, Application US/10278173 Publication No. US20030061637A1 GENERAL INFORMATION:
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Best Local Similarity 39.7%;
Matches 96; Conservative 3
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APPLICANT:
                    APPLICANT:
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APPLICANT: Ratcliffe, Oliver
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APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
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                                                                                                   APPLICANT:
APPLICANT:
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                               228 IG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKISDLKKTKDQIVKDVSFVTKFEETDKSGDQKQNKYIRNGLVCKEE---RVVVEEKIGP
                                                          Riechmann, Jose-Luis
Pineda, Omaira
Zhang, James
Yu, Guo-Liang
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Pilgrim, Marsha
Keddie, James
Heard, Jacqueline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 408; DB 11;
; Pred. No. 2.3e-31;
37; Mismatches 83;
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APPLICANT: Samaha, Raymond
TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
FILE REFERENCE: MBI-009
CURRENT APPLICATION NUMBER: US/10/278,173
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: US/09/533,392
PRIOR PILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 177
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 72
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US-10-278-173-72
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Best Local Similarity
Matches 96; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
               APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
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APPLICANT:
APPLICANT:
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APPLICANT: Creelman, Robert
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APPLICATION NUMBER: MBI-0023
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Jiang, Cai-Zhong
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Ti--hmann, Jose Luis
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Ratcliffe, Oliver
Adam, Luc
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Yu, Guo-Liang
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Ratcliffe, Oliver
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b. US20030121070A1
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RESULT 12
US-09-934-455-252
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-407-920-29
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                                                                                                             Sequence 252, Application US/09934455 Publication No. US20030121070A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.:
SEQ ID NO 390
LENGTH: 203
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Best Local Similarity
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APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
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TITLE OF INVENTION: MYS Transcription Factors
FILE REFERENCE: 38-21(52703)A
CURRENT APPLICATION NUMBER: US/10/407,920
CURRENT FILING DATE: 2003-06-06
CURRENT FILING DATE: 2003-06-06
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2002-04-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                             17 KKGLWTVEEDKILMDYVKAHGKGHWNRIAKKTGLKRCGKSCRLRWMNYLSPNVKRGNFTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 KKGLWTVEEDKILMDYVKAHGKGHWNRIAKKTGLKRCGKSCRLRWMNYLSPNVKRGNFTE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 RKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQ
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48.7%; Pred. No. 7.6e-31;
vative 26; Mismatches 49
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48.7%; Pred. No. 7.6e-31;
ative 26; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
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37;

Gaps

73 72

218 250 161

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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shi, June
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MyB-Related Transcription Factors
FILE REFERENCE: BB1280 US NA
CURRENT APPLICATION NUMBER: US/09/443,704
CURRENT APPLICATION NUMBER: 60/109,294
EARLIER APPLICATION NUMBER: 60/109,294
EARLIER FILING DATE: No. US20020066120Alember 20, 1998
NUMBER OF SEQ ID NOS: 50
SOFTMARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MB1-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MB1-0022
PRIOR APPLICATION NUMBER: MB1-0023
PRIOR APPLICATION NUMBER: MB1-0023
PRIOR APPLICATION NUMBER: MB1-0023
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
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US-09-443-704-12
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 107;
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Best Local Similarity 31.9%;
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSSEVGFGVDEELLDWEFQGNVTCQSDDLWDLSD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNLPPMQQGVQND----DFSAEI-----DLWNLLD
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Ratcliffe, Oliver
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Pred. No. 3.8e-30;
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US-10-008-118A-12
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Publication No. US20020187539A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription
FILE REFERENCE: BB1280 USDIV
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SOFTWARE: Microsoft Office
SEQ ID NO 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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TH: 302
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          251 LPPMQQG 257
                                                                                                                                                                           131 GEISTKIEIIKPORRKYFSSTMKNVTNNNVILDEEEHCKEIISEKOTPDASMDNVDPWWI 190
                                                                                                                                                                                                                                          73 EVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPR--EKINNKC 130
                                                                                                                                                                                                                                                                                                       14 KGAWTKEEDERLINYIKLHGEGCWRSLPKAAGLLRCGKSCRLRWINYLRPDLKRGNFTEE
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                                                                                         NLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQISHENWGEFSLN
                                                                                                                                  TPATTATATAVPS----ANSSKKINNNN
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                                                  NDINNNNNGFQLVSNSAYANTKIGTNLVAAEDS---NSSSGVTTEESVPHHQLNLDLSIG
                                                                                                                                                                                                                       EDELI INLHSLLGNKWSLIAARLPGRTDNEI KNYWNTHIKRKLYSRGIDPQTHRPLNASA
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37.2%; Pred. No. 3.6e-30;
ative 36; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                         26.8%; Score 396.5; DB 1 37.2%; Pred. No. 3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                          36; Mismatches
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133

73

218 250 161 Gaps

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Sequence 2, Application US/10093837

Publication No. US20030150011A1

GENERAL INFORMATION:
APPLICANT: Grotewold, Erich
APPLICANT: Dias, Anusha P.
APPLICANT: Dias, Anusha P.
APPLICANT: Braun, Edward L.
TITLE OF INVENTION: TRANGENIC PLANTS WITH ALTERED LEVELS OF PHENOLIC COMPOUNDS
FILE REFERENCE: 22727/04082

CURRENT APPLICATION NUMBER: US/10/093,837

CURRENT APPLICATION NUMBER: 60/274,629
PRIOR APPLICATION NUMBER: 60/274,629
PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1

SEQ ID NO 2
LENGTH: 363
TYPE: PRT
CORGANISM: maize ZmMyb-IF-35 protein
US-10-093-837-2
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Search completed: January 29, 2004, 20:18:24
Job time : 34 secs
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US-10-093-837-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.7%; Score 394; DB 12; Length 36 Best Local Similarity 33.0%; Pred. No. 8.1e-30; Matches 99; Conservative 56; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || ||
219 LPSQPQG 225
                                                                                                       239 LLAPE-SPKLEVGPDGSCMDSYSGPPSGESGCGSSGPSGDVAQDLDLDDDKAIMD-WDLM 296
                                                                                                                                                       217 LIHEEISPPLNIG-EGNSMQ--QGQISHENWGEFSLNLPPMQQGVQNDDFSAEIDLWNLL 273
                                                                                                                                                                                                            185 SVSTPRPQSDDCGTAQSEEEQAQASASGLTS-----DGHGPEEEEEEEDPLALSEEMVSA 238
                                                                                                                                                                                                                                                                 168 ----
                                                                                                                                                                                                                                                                                                              130 SKLPGGGK--RRGGRASRGAVVAAAKEKK---AKEKDDRGNSKVAEAEQQLRDTEDDDGG 184
                                                                                                                                                                                                                                                                                                                                                           118 TKIVPREKINNKCGEISTKIBIIKPQRRKYFSSTMKNVTNNNVILDEEEH------
                                                                                                                                                                                                                                                                                                                                                                                                                69 FEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK------LNT 117
::| |:|::|| ||||||||| ||||| ||::||||::| |:
70 ISEEEEDMIIKLHATLGNRWSLIAGHLPGRTDNEIKNYWNSHLGRRAADFRDGVVVDIDL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 VGLXKGRWTKEEDEVLARYIKEHGEGSWRSLPKNAGLLRCGKSCRLRWINYLRAGLKRGN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CKEIISEKQTPDASMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 363;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
January 29, 2004, 20:09:31; Search time 20 Seconds
(without alignments)
1917-511 Million cell updates/sec
Title:
Perfect score: 1477
Sequence:
1477
Sequence:
1 MNSTSMSSLGVRKGSWTDEE......QQGVQNDDFSAEIDLWNLLD 274
Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters:
283308
```

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
• Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4	u	N	_	No.	Result
377.5	378	378	379.5	386	386.5	387	88	388	389	390.5	394	396	397	397	397	400	401	402.5	403	403	404	408	423.5	503.5	524	532.5	535	542.5	Score	
25.6	25.6	25.6		26.1		26.2		26.3	26.3	•	26.7	•	•	26.9	•	•	27.1	27.3	•	27.3	•	27.6	•	•	•	36.1		36.7	Match' I	Query
236	294	267	232	280	274	321	. 325	256	265	273	273	198	271	267	266	193	203	226	257	246	264	269	249	139	212	249	248	246	Length I	
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RESULT 2
B96608
Byrobable transcription factor F25P12.92 [imported] - Arabidopsis thaliana (rouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001

### ALIGNMENTS

B 8	g &	B 8	8 8	Query Ma Best Loo Matches	RESULT 1 A96689 hypothetica C;Species: C;Date: 02- C;Accession R;Theologis Chin, C.W. ansen, N.F. Nature 408, A;Authors: C.A.; Li, J. Rizzo, M.; Wu A;Title: See A;Reference A;Reference A;Reference A;Residues: A;Genetics: A
168 C-KEIISEKQTPDASMDNVDPWWINLLE 194     ;   ;   ;	123 REKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNVVILDEEEH 167 	67 GDFEQDEVDLILRLHKLLGNRWSLIAGRLÞGRTANDVKNYWNTNLLRKLNTTKIVÞ 122 	7 SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR 66	Query Match 36.7%; Score 542.5; DB 2; Length 246; Best Local Similarity 52.4%; Pred. No. 1.3e-32; Matches 109; Conservative 26; Mismatches 52; Indels 21; Gaps 4;	RESULT 1 A96689 C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Catession: A96689 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.c. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Waiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Residues: 1-246 <sto> A;Cross-references: GB:AE005173; NID:g10092494; PIDN:AAG12894.1; GSPDB:GN00141 A;Map position: 1</sto>

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A; Gene: MYB90
C; Superfamily:
C; Keywords: tr
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Heference and analysis of chromosome 1 of the plant Arabidopsis.
A;Heference number: A86141; MUID:21016719; PMID:11130712
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T51687
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; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characte
                                                                                                                                                                                                                                                                                                                                 myb-related transcription factor MYB90 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: T51687
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C;Superfamily: Arabidopsis 28K leaf-specific
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A; Residues: 1-248 < STO>
                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-249 <KRA>
A;Cross-references: EMB
                                                                                                                                                                                                                              A; Reference number: Z14349;
A; Accession: T51687
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                                                                                                                                                 A; Experimental source:
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Best Local :
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               Matches
                                                                             Keywords: transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 NNKCGEI-----STKIEIIKPQRRKYFSSTMKNVTNNNVILDEBEHCKEIISEKQTPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHENWGEFSLNLPPMQQGVQNDDFSAEID-LWNLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DVNPPCLGL--NINNVC--DNSIIYNKDKKKDQLVN-----NLIDGDNMWLEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KMKKRDITPIPTTPALKNNVYKPRPRSF-----TVNN-----DCNHLNAPPKV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR
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                                                                                                                                                 EMBL:AF062915; PIDN:AAC83637
                               36.1%;
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                                                                                           28K leaf-specific myb-related
                                                                                                                                                                                                                                                 characterisation of the members MUID:9839469; PMID:9839469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID: 99954749;
                               Score 532.5; DB 2; Pred. No. 7.1e-32;
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                                                                                                                                                                                                                                                                                                                 R.;
                 Mismatches
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                                              Length 249;
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                 43;
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Maiti, R.; Marziali
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                                       RESULT 5

B96689

C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
C; Accession: B96689

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 A.; Ecker, J.R.; Palm,
Chung, M.K.; Conn, L.;
Hughes, B.; Huizar, L.
816-820, 2000
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R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members A;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51680
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myb-related transcription factor MYB75 [imported] C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Date: 18-Aug-2000 #sequence_revision; Accession: T51680
                                                                                                                                  NVDPWWINLLEN---CNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LNTTKIVPREK---INNKCGEIST--KIEIIKPQRRKYFSSTMKNVTNNN 159
                                                                                                                                                                                                                        SSLGVRKGSWIDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                              VILDEEEHCKEIISEKQTPDASMDNVDPWWI
                                                                DITPIPTTPALKNNVYKPRPRSFTVNNDCNHLNAPPKVDVNPP---
                                                                                                                                                                                                      SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVFVRAGLNRCRKSCRLRWLNYLKPSIKR
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                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                         35.5%;
                                                                                                                                                                                                                                                                                           48.3%;
                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                           Score 524; DB 2;
Pred. No. 2.4e-31;
NLIDGDNMWL
                                                                                                                                                                                                                                                                          Mismatches
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                                190

    Arabidopsis thaliana

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                                                                                                                                                                                                                                                                                                           Length 212;
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C.J.; Federspiel, N.A.; Kaul, S.; W Conway, A.B.; Conway, A.R.; Creasy,

02-Aug-2002 S.; White, (reasy, T.H.;

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Alonso, war, K.;

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A;Introns: 99/3
C;Superfamily: Arabidopsis myb-related protein 5; myb DNA-binding repeat homology C;Superfamily: Abrabidopsis myb-related protein 5; myb DNA-binding repeat homology transcription regulation C;Keywords: DNA-binding repeat homology <MYB1>
F;20-72/Domain: myb DNA-binding repeat homology <MYB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Li, S.F.; Santini, J.M.; Nicolaou, O.; Parish, R.W. FEBS Lett. 379, 117-121, 1996
A;Title: A novel myb-related gene from Arabidopsis th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE005173; NID:g10092496; PIDN:AAG12896.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 15-Nov-1996 #sequence_revision 27-Feb-1997 #text_change
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C;Superfamily: Arabidopsis myb-related protein Y19; myb
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A; Residues: 1-139 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U26935; NID:g1254994; PIDN:AAC49311.1; PID:g1218000
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A; Residues: 1-249 <L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: A novel myb-related gene from Arabidopsis thaliana. A;Reference number: S68688; MUID:96225952; PMID:8635574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myb-related protein 5 - Arabidopsis thaliana
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Best Local
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                                                                                                                                                                                                                                                 Matches 100;
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Best Local
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  136
                                      127
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                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                      SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                      NNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEE-----HCKEIISEKQTPDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKFSSDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKK----
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                                                                               GGITSDEEDLILRLHRLLGNRWSLIAGRIPGRTDNEIKNYWNTHLRKKLLRQGIDPQ---
                                                                                                                                                                   TKMGMKRGPWTVEEDEILVSFIKKEGEGRWRSLPKRAGLLRCGKSCRLRWMNYLRPSVKR
                                                                                                                        GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Landsberg
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Pred. No. 4.6e-30;
                                                                                                                                                                                                                                                 Mismatches
  THKPLDANNIHKPEEEVSGGQKYPLEPISSSHTDDT 171
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                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                 65;
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A;Map position: 2
A;Introns: 88/2
A;Introns: 88/2
C;Superfamily: barley myb-related protein 1; myb DNA-binding C;Keywords: DNA binding; duplication; nucleus; transcription F;9-61/Domain: myb DNA-binding repeat homology <a href="Million: Myb DNA-binding repeat">MYBI></a>
F;62-112/Domain: myb DNA-binding repeat homology <a href="Million: Myb DNA-binding repeat">MYBI></a>
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A;Residues: 1-269 <QUA>
A;Cross-references: EMBL:X90385; NID:g928968; PIDN:CAA62033.1; PID:g928969
A;Cossidue S; Crossidue S; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.; I
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.,
euss, D.; Merman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 199
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: At2g16720
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A; Residues: 1-269 <STO>
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                                                                                                                                DINLELRISPPWONQREISTCTASRFYMENDMECSSETVKCQTENSSSISYSSIDISSSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVP--REKINN 128
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                                                                                                                                                                                                    DASMD-NVDPWWINLLE--NC-----NDDIEEDEEVVINYEKTLTSLLHEEIS-PPLN
                                                                                                                                                                                                                                                                    AKISDLKKTKDQIVKDVSFVTKFEETDKSGDQKQNKYIRNGLVCKEE---RVVVEEKIGP
                                                                                                                                                                                                                                                                                                                                        -KCGEI-STKIEIIK------PQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEGNSMQQGQISHENWGEFSLNLPPMQQGVQNDD 262
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250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
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n biosynthesis regulatory Zea mays (maize)

protein

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C;Date: 23-Apr-1999 #sequence_revision 23-A
C;Accession: T03974
R;Cone, K.C.; Cocciolone, S.M.; Moehlenkamp
Plant Cell 5, 1807-1816, 1993
A;Title: Role of the regulatory gene pl in
A;Reference number: Z15034; MUID:94138244;
A;Accession: T03974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable transcription factor MYB3 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: T51631 R;Kranz, H.D.; Denekamp, M.; R;Kranz, H.D.; Denekamp, M.;
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A;Title: Towards functional characterisation of the members A;Reference number: Z14349; MUID:9839469; PMID:9839469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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F;9-61/Domain: myb DNA-binding repeat homology <MYB1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:L19496; NID:g309571; PIDN:AAA19819.1; PID:g309572
A;Experimental source: strain Tx303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF062859; PIDN:AAC83581.1
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z14349;
A; Accession: T51631
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                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-246 < KRA>
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                        Superfamily: barley myb-related protein 1; myb DNA-binding repeat;
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Best Local
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                                                                                           CGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCK-EIISEKQTPDASMDNVDPW
                                                                                                                              EEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLLSRGIDPNSHRLINE
                                                                                                                                               MNKGAWTKEEDQLLVDYIRKHGEGCWRSLPRAAGLQRCGKSCRLRWMYYLRPDLKRGNFT
                                                                                                                                                                                                                         VRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFE
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 - IGMVNNCESSGTTSEKDYGNEEDWVLNLELSVGPSYRYESTRKVSVVDSAE---
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                              -DIEEDEEVVINYEKTLTSLLHEERSPLNIGEGNSMQQGQISH
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                                                                                                                                                                                                                                                                         Score 403; DB 2;
Pred. No. 2.1e-22;
                                                               -SSLQNDVVETIHLDFSGPVKPEPVREE
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     A;Cross-references:
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A;Map position: 1
A;Introns: 45/1; 88/2
A;Introns: 45/1; 88/2
C;Superfamily: barley myb-related protein 1; myb DNA-binding C;Keywords: DNA binding; duplication; nucleus; transcription C;Keywords: DNA binding; duplication; protein 1; myb DNA-binding repeat homology cMYBly
E;9-61/Domain: myb DNA-binding repeat homology cMYBly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AC003979; NID:g3172156; PIDN:AAC25522.1; PID:g32694; GSPDB:GN000
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                  A; Description: Structure a. A; Reference number: Z16842 A; Accession: T09773
                                                                                                                  R;Loguercio, L.L.; Zhang, u.; marane, submitted to the EMBL Data Library, November 1997
                                                                                                                                                                                                                   myb-related protein - upland cotton
N;Alternate names: MYB-like DNA-binding domain protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #te:
                    A; Molecule type: mRNA
A; Residues: 1-226 < LOG>
                                                           A; Status: preliminary; translated
                                                                                                                                                                                              C; Accession: T09773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;62-112/Domain: myb DNA-binding repeat homology <MYB2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-257 < VYS>
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A; Accession: T00780
                                                                                                                                                                                                                                                                                                                                                                                                   217 RRWG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -IGMVNNCESSGTTSEKDYGNEEDWVLNLELSVGPSYRYESTRKVSVVDSAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLLSRGIDPNSHRLINE 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 403; DB 2;
Pred. No. 2.2e-22;
11; Mismatches 68
                                                                from
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NID:g2921339; PID:g2921340
                                                                  GB/EMBL/DDB:
                                                                                                                                                                                                                     16-Jul-1999 #text_change
                                                                                                                                  classes
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EMBL:AF034134;

source:

cultivar

Acala

SJ-2; ovule

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A;Note: Cmy-O
C;Superfamily: 1
C;Keywords: DNA
F;8-60/Domain: 1
RESULT 13
T109744
T109744
myb-related protein - upland cotton
myb-related names: MYB-like DNA-binding domain protein
N;Alternate names: MYB-like DNA-binding domain protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: protein T9L3_50
C;Speciles: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: T51420
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tal submitted to the Protein Sequence Database, August 2000
                                                                                                                                                                                                                                                                            8
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A;Note: T913_50
C;Superfamily: trichome differentiation protein GL1; myb DNA-binding repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: cultivar Columbia; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-203 <SAT>
A;Cross-references: EMBL;AL391149
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A; Accession: T51420
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Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Experimental;Genetics:
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                                                                                                                                                                                                                                                                                                                                                        RKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D---LDLTIAFPSSPIKNI---IEESQQKTASIVTNDEEEQYTVPTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNQYPHHVGPLNPTTTNSMDVACKLRVCSTDNDDGISDAASYL----EDATPPTGISNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKINNK
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                                                                                                                                                               DIVYQINLPNPTETSEETKISNIVDNNNILGDEIQEDH
                                                                                                                                                                                                   EISTKIEIIKPORRKYFSSTMKNVTNNNVILDE--EEH
                                                                                                                                                                                                                                                                                                                      KKGLWTVEEDKILMDYVKAHGKGHWNRIAKKTGLKRCGKSCRLRWMNYLSPNVKRGNFTE
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                                                                                                                                                                                                                                                                                                                                                                                                                   27.1%; Score 401; DB 2; 48.7%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.3%; Score 402.5; DB 2; 41.7%; Pred. No. 2.1e-22;
                                                                                                                                                                                                                                         LGNRWSLIAKRVPGRTDNQVKNYWNTHLSKKLG
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ches 66;
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EQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK

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A;Description: transcriptional activator for anthocyanin biosynthesis C;Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-b: F;9-61/Domain: myb DNA-binding repeat homology KTB>
                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T03972
R;Cone, K.C.; Cocciolone, S.M.; Moehlenkamp, C.A.; Weber, T Plant Cell 5, 1807-1816, 1993
A;Title: Role of the regulatory gene pl in the photocontrol A;Reference number: Z15034; MUID:94138244; PMID:8305873
A;Accession: T03972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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A;Experimental source: cultivar Acala SJ-2; ovule
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T09744
R;Loguercio, L.L.; Zhang, J.; Wilkins, T
submitted to the EMBL Data Library, Nove
A;Description: Structure and expression
밁
                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:L19495; NID:g309569; PIDN:AAA19821.1; A;Experimental source: strain McClintock
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                                                                                                                                                                                                                                                   A; Introns:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                        A;Gene: pl
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                                                                                                                                                     ;62-112/Domain:
                                                                                                                                                                                                                                                                                          ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Zea mays (maize)
Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999;
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                                                                            Matches
                                                                                          Query Match
Best Local
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                                                                                              Similarity
  GVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCGKSCRLRWLNYLRPNI KRGNI
                                    GVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KINNKCGEISTK-----IEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRGNISDQEEDLILRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNSHLSKKVN-----QKE
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                                                                          Conservative
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                                                                                                                                                     DNA-binding
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                                                                                            26.9%;
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brary, November 1997
expression of six classes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Mismatches
                                                                                                                                                   repeat
                                                                        Score 397; DB 2;
Pred. No. 6.4e-22;
4; Mismatches 20
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Pred. No. 2.6e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 6
A;Introns: 45/1; 88/2
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anthocyanin biosynthesis regulatory protein Pl - maize
N;Alternate names: Pl transcription factor
C;Species: Zea mays (maize)
C;Date: 12-Feb_1999 #sequence_revision 12-Feb-1999 #text_change 13-Aug-1999
C;Date: 12-Feb_1999 #sequence_revision 12-Feb-1999 #text_change 13-Aug-1999
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submitted to the EMBL Data Library, July 1997
A;Description: Pl-987: a nonfunctional maize anthocyanin regulatory gene resulting from
A;Reference number: Z14257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Molecule type: DNA; Residues: 1-267 <COO>; CTOOS - references: EMBL:AF015268; NID:g2343272; PIDN:AAB67720.1; PID:g2343273; Experimental source: cultivar W22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: T01188
                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.9%; Score 397; DB 2; Length 267; Best Local Similarity 67.6%; Pred. No. 6.4e-22; Matches 71; Conservative 14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                      10 GVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDF 69
                                                                                                                                                             70 EQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK 114
                                                                                                                                                                                                                                                      11 GVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCGKSCRLRWLNYLRPNIKRGNI 70
                                                                                                                               71 SYDEEDLIVRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNSTLGRR 115
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Title:
Perfect score:
Sequence: OM protein - protein search, using sw model Run on: US-10-033-190-2 1477 1 MNSTSMSSLGVRKGSWTDEE.....QQGVQNDDFSAEIDLWNLLD 274 January 29, 2004, 20:04:26; Search time 18 Seconds (without alignments) 715.851 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Scoring table:

Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_41:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	s	4	ω	2	_	Result No.
108	127.5	137	142.5	167	185.5	221.5	235	235.5	236.5	236.5	236.5	237.5	240.5	241	242.5	242.5	248.5	252	255	261.5	262	263	339.5	343	361	362	363	365	378	394	395	411.5	Score
7.3	8.6	9.3	9.6	11.3		'n	15.9	15.9	6	٠	16.0		16.3	16.3	16.4	16.4	16.8	17.1	17.3	17.7	17.7	17.8	•	23.2	•	24.5	•	•	٠	26.7	26.7	27.9	Query Match I
595	449	590	811	757	229	451	367	382	641	640	636	757	640	624	752	751	728	657	686	700	704	743	302	421	228	399	255	340	267	273	252	258	Length DB
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	022928					P25588	Q54807	Q53770	P21598	P21538	Q8k9t8
haemophilus	arabidopsis	thermotoga	plasmodium	neisseria m	enterococcu	saccharomyc	streptococc	staphylococ	enterococcu	saccharomyc	buchnera ap

# ALIGNMENTS

	R R R R R R R R R R R R R R R R R R R	RESULT TT2_AR TT2_AR ATC CO ATC CO ATC CO ATC CO ATC CO ATC CO ATC ATC ATC CO ATC
MEDLINE-21481677; PubMed=11597504; Stracke R., Werber M., Weisshaar B.; "The RZB3-MYB gene family in Arabidopsis thaliana."; Curr. Opin. Plant Biol. 4:447-456(2001). [3] SEQUENCE FROM N.A. STRAIN-CV. Columbia, MEDLINE-99087489; PubMed=9872454; MEDLINE-99087489; PubMed=987244; MEDLINE-	SEQUENCE FROM N.A., AND MUTANTS TT2-2 AND TT2-4.  STRAIN=cv. Columbia, cv. Landsberg erecta, and cv. Wassilewskija;  MEDLINEs-21434422; pubwde-41549766;  Wesi N., Jond C., Debeaujon I., Caboche M., Lepiniec L.;  "The Arabidopsis TT2 gene encodes an R2R3 MYB domain protein that acts as a key determinant for proanthocyanidin accumulation in developing seed.";  Plant Cell 13:2099-2114(2001).  SEQUENCE FROM N.A.	ARATH ARATH ARATH STANDARD; PRT; 258 AA.  QPTJA; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) TRANSPARENT TESTA 2 protein (Myb-related protein 123) (AtmyB123) (Myb-related transcription factor LBM2-like) TP2 OR MYB123 OR AT5G35550 OR MOK9.18. Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  [1]  [1]  [1]  [28 AA.  [29 AA.  [20 AA.  [20 AA.  [21 AA.  [21 AA.  [22 AA.  [23 AA.  [24 AA.  [25 AA.  [26 AA.  [26 AA.  [27 AA.  [27 AA.  [27 AA.  [28 AA.  [28 AA.  [27 AA.  [28 AA.  [28 AA.  [27 AA.  [28 AA.  [28 AA.  [28 AA.  [29 AA.  [27 AA.  [28 AA.  [28 AA.  [27 AA.  [28 AA.  [28 AA.  [27 AA.  [28 AA.  [27 AA.  [27 AA.  [27 AA.  [27 AA.  [28 AA.  [27 AA.  [27 AA.  [27 AA.  [27 AA.  [28 AA.  [27 AA.  [28 AA.  [29 AA.  [20

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RESULT 2
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NP BIND
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01-NOV-1991
28-FEB-2003
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EMBL; AB015477; BAB
HSSP; P06876; IMBK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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EMBL; AF371981; AAK54744.1; -.
EMBL; AB015477; BAB08716.1; -.
                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
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                            MEDLINE=90151603; PubMed=2303027; Paz-Ares J., Ghosal D., Saedler H.; "Molecular analysis of the C1-I allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGEN
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of the regulatory 9:315-321(1990).
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                                                                                                                                                                                                                                                                                                                           STANDARD;
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54
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Q -> L (IN CV. WS).

G->R: IN TT2-4; LOSS O
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MISSING: IN TT2-2; RED
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Pred. No. 2.
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PROSITE; PS00037; MYB 1; 1.
PROSITE; PS0034; MYB 2; 1.
PROSITE; PS50034; MYB 3; 2.
Nuclear protein; DNA-binding; Repo
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P10290;
01-MAR-1989
01-MAR-1989
28-FEB-2003
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DNA BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                     MAIZE
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EMBO J. 6:3553-3558(1987),

-I- FUNCTION: CONTROLS THE EXPRESSION OF GENES
BIOSYNTHESIS. REGULATES THE EXPRESSION OF A
GENES: CHALCONE SYNTHASE, DITYDROFLAVONOL R
O(3) GLUCOSYLTRANSFERASE. C1 ACTS AS A TRAN
                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; SpacCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                   to myb
                                                                                     Paz-Ares J., Ghosal D., Wienand U., Peterson P.A., Saedler H.; "The regulatory c1 locus of Zea mays encodes a protein with homology to myb proto-oncogene products and with structural similarities to
                                                                                                                                                                      NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activator;
                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=88111545; PubMed=3428265;
                                                                                                                                                                                                                                   Zea mays (Maize)
                                                                                                                                                                                                                                                                Anthocyanin
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P01103; 1POM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203
252 AA;
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(Rel.
(Rel.
                                                                                                                                                                                                                                                              regulatory
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                                                                                                                                                                                                                                                                                                                                      STANDARD;

    Last sequence u
    Last annotation

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212
26419
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                                                                                                                                                                                                                                                                protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 395; DB 1;
Pred. No. 4.4e-22;
6; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYB 1.
MYB 2.
POLY-GLY.
, AD61FA2B829C5FBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
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                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                       273
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                                                                                                                                                                                                                                                                             update)
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                 S INVOLVED IN ANTHOCYANIN
AT LEAST 3 STRUCTURAL
REDUCTASE AND FLAVONOL
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    AND FLA
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between
                                                                                                                            Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                      MYB1_HORVU
P20026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001005; Myb DNA_binding.
Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
SMART; SM00717; MYB 1; 1.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00034; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
Nuclear protein; DNA-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M37153; AAA33482.1; PIR; S06215; TVZMMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                             01-FEB-1991
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                              HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                        Salamini F., Rohde W.;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                            NCBI_TaxID=4513;
                                                                                                                                                                                                                                                            MYB1.
                                                                                                                                                                                                                                                                       Myb-related
             Wissenbach M., Rohde W.;
                                   STRAIN=cv. Abyssinian 2231; TISSU
MEDLINE=94035190; PubMed=8220488;
                                                 STRAIN=cv.
                                                                                   "Multiple genes are transcribed in Hordeum vulgare and Zea mays carry the DNA binding domain of the myb oncoproteins."; Mol. Gen. Genet. 216:183-187(1989).
                                                                                                                                                                                                             Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                 16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activator; Trans-acting factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MaizeDB; 24964; -
                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear (Probable). SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
genes from Hordeum vulgare: tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P01103; 1POM.
                                                                                                                                                                                                                                                                                                                                                                                               71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                             SYDEEDLIIRLHRLLGNRWSLIAGRLPGRTDNEIKNYWNSTLGRR 115
                                                                                                                                                                                                                                                                                                                                                                                                            EQDEVDLILERLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                            GVKRGAWTSKEDDALAAYVKAHGEGKWREVPOKAGLRRCGKSCRLRWLNYLRPNIRRGNI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDF 69
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205
234
273 A
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(Rel. 17
(Rel. 40
protein
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                        Ueberlacker B.,
                                                                                                                                                                                                                                                                                                                                   STANDARD;
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40, La
in Hv1.
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Last sequ
                                                2231; TISSUE=Leaf;
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                                                                                                                                                                                                                      Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                              sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-GLY.
ASP/GLU-RICH (ACIDIC).
, 163977BBA8CE669D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 394; DB 1;
Pred. No. 5.8e-22;
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                        Vogt F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                  267
                                                                                                                                   Paz-Ares
                                                                                                                                                                                                                                                                                update)
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                        Becker D.,
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                        Salamini
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Best Local S
Matches 73
                                                                                                                                                                       01-FEB-1991
01-FEB-1991
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                        MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb
or send an email to license@isb-sib.ch).
                                 MEDLINE=89313655; PubMed=2664447; Marocco A., Wissenbach M., Becker D., Salamini F., Rohde W.;
                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
PACCAD clade; Panicoideae; Andropogoneae;
                                                                                                                                                            Myb-related
                                                                                                                                                                                                              MYB1_MAIZE
P20024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X70877; CAA50222.1; -. EMBL; X70879; CAA50224.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimeric Myb promoter/Gus genes in transgenic tobacco.";
"Multiple genes are transcribed in Hordeum vulgare and carry the DNA binding domain of the myb oncoproteins.", Mol. Gen. Genet. 216:183-187(1989).
                                                                       SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=4577;
                                                                                                                                   Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S61506; S61506.
HSSP; P01103; 1POM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright.
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                                                                                                                                                Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T02887; -.
InterPro; IPR001005; Myb_DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOSYNTHESIS.
SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: GERMINATING SEED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 2 Myb-like domains.
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                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                131
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                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                     AASNITISFESAQR 147
                                                                                                                                                                                                                                                                                                                                                    EVDLILRLHKILGNRWSLIAGRLFGRTANDVKNYWNTNLLRKLNTTKIVF--REKINNKC 130
                                                                                                                                                                                                                                                                                                                                                                                                       KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD 72
                                                                                                                                                                                                                                                                                                                GEISTKIEIIKPOR 144
                                                                                                                                                                                                                                                                                                                                        EDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLTSRGIDPVTHRAINSDH
                                                                                                                                                                                                                                                                                                                                                                                         KGAWTKEEDDRITAYIKAHGEGCWRSLPKAAGILRCGKSCRLRWINYLRPDLKRGNFSHE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
62
267 AA;
                                                                                                                                                           (Rel. 17, Created)
(Rel. 17, Last sequence up
(Rel. 41, Last annotation
protein Zml.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                           STANDARD;
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112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 378;
Pred. No. 8.
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MYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Bioinformatics and the
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                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                      update)
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IN THE REC
                                                                                                                                                                                                                           340
                                              Paz-Ares
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                                                                                                                                                                         update)
                                                                                                                                   Embryophyta; Tracheophyta;
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                                                                                                            Poales;
Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
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                                              J.,
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OF FLAVONOID
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Best Local S
Matches 94
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SMART; SM007017; SANT; ...

PROSITE; PS00037; MYB 1; 1.

PROSITE; PS00034; MYB 3; 2.

PROSITE; PS50090; MYB 3; 2.

Nuclear protein; DNA-binding; Repeat; Transcription regulation.

NNA BIND 11 63 MYB 1.

NNA BIND 64 114 MYB 2.

NNA BIND 64 114 MYB 2.

C729 MW; F2341387F6263DAF CRC64;
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01-FEB-1991
01-FEB-1991
28-FEB-2003
                                                                                                                                     "Multiple genes are transcribed in Hordeum vulgare and carry the DNA binding domain of the myb oncoproteins.";
Mol. Gen. Genet. 216:183-187(1989).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 2 Myb-like domains.
PIR; S04899; S04899.
HSSP; P01103, 1POM.
TRANSFAC; T02959; -.
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Zea mays (Maize)
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   InterPro; IPR001005; Myb DNA binding. Pfam; PF00249; myb DNA-binding; 2. SMART; 8. SMART; 8. SMART; 8. SMART; 8. SMART; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marocco A., Wissenbach Salamini F., Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=89313655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4577;
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nbach M., Becker D.,
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Pred. No. 9.9e-20;
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01-AUG-1992 (Rel
28-FEB-2003 (Rel
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          EMBL; M73028; AAA33500.1; -.
EMBL; M73029; AAA33501.1; -.
CAA77939.1; -.
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PROSITE; PS50090; MYB_3; 2.
Nuclear protein; DNA-binding;
                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               Grotewold E., Athma P., Peterson T.; "Alternatively spliced products of the maize P gene with homology to the DNA-binding domain of myb-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=91271238; PubMed=2052542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myb-related
                                                                                                   between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The Buropean Broading institutions as longues by non-profit institutions as longues.
                                                                                                                                                                                                                                                                                                                                       Athma P., Grotewold E., Peterson "Insertional mutagenesis of the r
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92275319;
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                Genetics 131:199-209(1992).
                                                                                                                                                                                                                                                                                                                              transposition
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                   IsoId=P27898-2; Sequence=VSP_003301, VSP_003302;
SIMILARITY: Contains 2 Myb-like domains.
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255 AA;
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112 M
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Pred. No. 9.7e
L4; Mismatches
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PP7900; Q9ST42;
01-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Trichome differentiation protein GLI (GLABROUSI protein).
GLI OR AT3G27920 OR K16N12.17.
GLI OR AT3G27920 OR K16N12.17.
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=92034971; PubMed=1934056;

Oppenheimer D.G., Herman P.L., Sivakumaran S., Esch J.,

P. myb gene required for leaf trichome differentiation
is expressed in stipules.";

Cell 67:483-493(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
Nuclear protein; DNA-Binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00249; myb DNA-binding; SMART; SM00717; SANT; 2.
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TRANSFAC; T01591; -.
MaizeDB; 69180; -.
MaizeDB; 69181; -.
InterPro; IPR001005; Myb_DNA_binding.
                                                                                                                                             Shikazono
                                                                                                                                                              STRAIN=cv. Columbia;
MEDLINE=99449058; PubMed=10520748;
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                              Shikazono N., Tanaka A., Yok
"Nucleotide sequence of the
ecotype Columbia.";
DNA Seq. 9:177-181(1998).
                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                   FROM N.A.
v. Columbia,
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9 61
62 112
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                     ÇV.
                   Ba-1,
                                                                                                                                               Yokota Y.,
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                                                                                                                         GLABROUS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 362; DB 1
Pred. No. 2e-19;
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MYB 2.
POLY-ALA.
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/FTId=VSP_003302.
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                     ÇV.
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                   Bla-1,
                                                                                                                     Watanabe H., Tano S.;
S1 gene of Arabidopsis thaliana
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                     CV.
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                   Cond,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hauser M.T., Harr B., Schlotterer C.; "Trichome distribution in Arabidopsis thaliana and its close Arabidopsis lyrata: molecular analysis of the candidate gene GLABROUS1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20363099; PubMed=10907853;
Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., 7
"Structural analysis of Arabidopsis thaliana chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
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InterPro; IPR001005; Myb
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BAC clones.";
Res. 7:217-221(2000).
FUNCTION: REGULATES THE PRODUCTION
FUNCTION: PRECURSOR CELLS ON
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; AF263990; AAL01218.1; -...

L; AF263693; AAL01218.1; -...

L; AF263694; AAL01219.1; -...

L; AF263695; AAL01220.1; -...

L; AF263696; AAL01221.1; -...

L; AF263697; AAL01222.1; -...

L; AF263697; AAL01222.1; -...

L; AF263697; AAL01223.1; -...

L; AF263697; AAL01223.1; -...
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P01103; 1POM.
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; PS00037; MYB 1; 1.

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; PS5090; MYB 3; 2.
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LAQKDVLMATTN--DPSHYYGNNALWVH-----DDDFELSSLVMMNF
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149
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Inding; 2.
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C -> R
GDV ->
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Pred. No. 1
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DV -> SDI (IN REF.
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RESULT 10
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P80073;
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DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Physcomitrella patens (Moss).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHYPA
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-I- FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR.
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MEDLINE=94004988; PubMed=8401607;
M.T. Kammerer W., Cove D.J., I
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28-FEB-2003
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PIR; S24244; S24244.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear (Potential).
DEVELOPMENTAL STAGE: HIGH RATES OF GROWTH.
SIMILARITY: Contains 2 Myb-like domains.
                                                                                            183
                                                                                                                      130
                                                                                                                                               129
                                                                   190
                                                                                                                                                                         70
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                                                                                                                                                                                                                                                                               80;
                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                 PS00037; MYB 1; 1.
PS00334; MYB 2; 1.
PS50090; MYB 3; 2.
Protein; DNA-Dinding; Repeat;
                                                                                                                                                                                                                                            LGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGD
                                                                   CQSDEGPVLLKVPKAPKSPISVNPGPGCNYDDDSEH---
                                                                                               DNVD-----
                                                                                                                       EDSKLDDTEDDTDDEGGDSSDVTMSDASKSEKRSKKKSKPKETVKVRQPKGPKPAPQLKM
                                                                                                                                               KCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEBEHCKEIISEKQ-----TPDASM
                                                                                                                                                                         FSEAEENLILDLHATLGNRWSRIAAQLPGRTDNEIKNYWNTRLKKRLRSQGLDPNTHLPL
                                                                                                                                                                                                  FEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKINN
                                                                                                                                                                                                                             VGLRRGPWTSEEDQKLVSHITNNGLSCWRAIPKLAGLLRCGKSCRLRWTNYLRPDLKRGI
                                                                                                                                                                                                                                                                                                                                 421
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(Rel. 28
(Rel. 41
protein
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                               62
9
                                                                                                                                                                                                                                                                                                                                 AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
     STANDARD;
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. 41, Last r
rein Pp2.
                                                                                                                                                                                                                                                                                                                                               61
112
                                                                                                                                                                                                                                                                                                                                 L12
MYB 2.
46695 MW; 27A3578578D0F3F4 CRC64;
                                                                                                                                                                                                                                                                                          23.2%;
                                                                                             -----PWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                               Score 343; DB
Pred. No. 5.2e
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                           EXM
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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     302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                     Transcription
                                                                                                                                                                                                                                                                                           DB 1;
5.2e-18;
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Physcomitrella
                                                                                                                                                                                                                                                                                                       Length 421;
                                                                     -SSSSTVTTKSHED
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                     regulation;
                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patens.";
                                                                     238
                                                                                               221
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                               182
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                                                                                         Matches
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Best Local
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01-JUN-1994
16-OCT-2001
                                                                                                                                          Repeat.
DNA_BIND
DNA_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                       SMART; SM00717; SANT; 2.
PROSITE; PS00037; WYB 1; 1.
PROSITE; PS00334; WYB 2; 1.
PROSITE; PS50039; WYB 3; 2.
Nuclear protein; DNA-Dinding;
                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Multiple genes are transcribed in Hordeum vulgare and carry the DNA binding domain of the myb oncoproteins.", Mol. Gen. Genet. 216:183-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marocco A., Wissenbach M., Becker D., Paz-Ares J., Salamini F., Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                       EMBL; X70881; CAA50226.1;
EMBL; X70878; CAA50223.1;
PIR; S31818; S31818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chimeric Myb promoter/Gus
Plant J. 4:411-422(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Abyssinian 2231; TISSUE=Leaf;
MEDLINE=94035190; PubMed=8220488;
                                                                                                                                                                                                                                                                                    TRANSFAC; T02889; -. InterPro; IPR001005;
                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89313655; PubMed=2664447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 35-302 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myb-related
                                                                                                                                                                                                                                                                         Pfam; PF00249; myb_DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR IN RESPONSE EXTERNAL SIGNAL. MAY BE INVOLVED IN THE REGULATION OF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Abyssinian 2231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myb genes from Hordeum vulgare: tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wissenbach M., Ueberlacker B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                            HSSP; P01103; 1POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear (Probable) TISSUE SPECIFICITY: GERMINATING SEED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOSYNTHESIS.
             58
                                                                                         67; Conserv
NYLRPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNT 117
                                       MGRPSSGAVGQPKVRKGLWSPEEDEKLYNHIIRHGVGCWSSVPRLAALNRCGKSCRLRWI
                                                               MNSTSMSSLG---VRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWL 57
                                                                                                                                          302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 17, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                          Conservative
                                                                                                                                                                     64
                                                                                                                                                       63
114
259
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                                                                                                                                            33003
                                                                                                     23.0%;
                                                                                                                                                                                                                                                                                     Myb_DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes
                                                                                                                                            MW;
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                                                                                          16;
                                                                                                                                                       MYB 1
                                                                                                       Pred.
                                                                                                                  Score 339.5;
                                                                                                                                            A -> P (IN REF. 2).
89017418C3631599 CRC64;
                                                                                                                                                                                                           Activator;
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                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the myb oncoproteins.";
                                                                                                       No. 6.2e-18
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                                                                                                                                                                                                                                                                                                                                                                                           oved. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                           is produced through a collaboration -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND
                                                                                                                                                                                                           Transcription regulation,
                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APICAL MERISTEM OF SHOOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tobacco.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression
                                                                                                                  Length
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saedler H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salamini
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                                                                                                                     302;
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RESULT 11
MYBB XENLA
ID MYBB XENLA
AC P52551;
DT 01-OCT-1996
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                                                                     Query Match
Best Local
                                                             Matches
                                                                                                                                      Pfam; PF00249; myb DNA-bInding; 3
SWART; SW00717; SANT; 3.
PROSITE; PS00037; MYB_1; 3.
PROSITE; PS00034; MYB_2; 3.
PROSITE; PS50090; MYB_3; 3.
PROSITE; PS50090; MYB_3; 3.
                                                                                                   DNA_BIND
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJINE=92297434; PubMed=1606020;
Bouwmeester T., Guehmann S., El-Baradi T., K
van Wijk I., Moelling K., Pieler T.;
"Molecular cloning, expression and in vitro
characterization of Myb-related proteins in
Mech. Dev. 37:57-68(1992).
                                                                                                                                 DNA
                                                                                                                                                                                                                                                      modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
                                                                                                                                                                                                               EMBL; M75870; AAC98701.1;
HSSP; Q03237; 1A5J.
                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                               Humbert-Lan G., Pieler T_{\cdot,\cdot} "Regulation of DNA binding activity and
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99214591; PubMed=10187816;
Humbert-Lan G., Pieler T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS TO C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myb-related protein B
MYBL2 OR BMYB OR MYB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000
15-SEP-2003
                                                                                                                                                                                           InterPro; IPR001005; Myb_DNA_binding,
Pfam; PF00249; myb_DNA-binding; 3.
                                                                                                                                                                                                                                                                                                                                                                                Xenopus oocytes.
J. Biol. Chem. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenopodinae;
                                                                                                                                 BIND
                                                                                                                                                                                                                                                              European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content if ited and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 3 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: PRESENT THROUGHOUT OOGENESIS AND EARLY XENOPUS EMBRYOGENESIS; IN ADULT TISSUE IT IS PRIMARILY DETECTED
                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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 73
                     83
                                        13
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGIDP 125
 EVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIV-----PR 123
                     KGPWTKEEDEKVIELVKKYGTKHWTLI-AKQLRGRMGKQCRERWHNHLNPEVKKSSWTEE
                                        KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYLRPDLKRGCFSQQEEDHIVALHQILGNRWSQIASHLPGRTDNEIKNFWNSCIKKKLRQ 120
                                                                                                130
743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 39, (Rel. 42,
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus.
                                                                                                    A
A
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                                                                                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9, Last sequence update)
2, Last annotation updat
B (B-Myb) (Myb-related
                                                                                                                                   77
                                                                                                    82909 MW;
                                                                      31.9%;
                                                                               17.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                         Nuclear protein;
                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a; Craniata; Vertebrata; Mesobatrachia; Pipoidea;
                                                                                                           MYB 2.
                                                           Score 263; DB 1;
Pred. No. 7.2e-12;
6; Mismatches 8:
                                                                                                                                 MYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             notation update)
(Myb-related pr
                                                                                                   5FD1D678BB24409B CRC64;
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                                                                                                                                                                                                                                                      (See
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                                                                                                                                                                                                                                                      http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 1) (XMYB1)
                                                                                                                                          DNA-binding; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalkbrenner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       functional
                                                            83;
                                                                              Length
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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                                                                                743;
                                                            28;
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                                                            Gaps
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MYBB_MOUSI
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       MOD_RES
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P48972;
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                            MOD_RES
                                                                                                                                                             HSSP;
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                                                                                Franscri
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Phosphorylation.
DNA_BIND 26
DNA_BIND 78
DNA_BIND 130
                                                           DNA_BIND
                                                                                                                                PROSITE; PS00037; MYB_1; 3. PROSITE; PS000334; MYB_2; 3. PROSITE; PS50090; MYB_3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                         EMBL; X70472; CAA49898.1;
EMBL; X73028; CAA51511.1;
                                                                                                                                                                                                                                                                                                                                                    modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92366176; PubMed=1501895;
Lam E.W., Robinson C., Watson R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYBL2 OR BMYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996
                                                                                                                                                                                  SMART; SM00717;
                                                                                                                                                                                             InterPro; IPR001005; Myb_DNA_binding;
                                                                                                                                                                                                                                                          PIR; S33704; S33704.
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse B-myb transcription.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lam E.W., Watson R.J.;
"An E2F-binding site mediates cell-cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 7:1885-1890(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                            MGD; MGI:101785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93327760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-6 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization and cell cycle-regulated
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SIMILARITY: Contains 3 Myb-like domains.
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MYB 2.
MYB 3.
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Institute. There are
SIMILARITY)
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Mammalia; Eutheria;
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                                                                                                                                                         Nucleic
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MEDLINE=89083548; PubMed=3060855;
Nomura N., Takahashi M., Matsui M.,
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01-MAR-1989
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Primates;
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Catarrhini; Hominidae,
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GO; GU:... InterPro;

GO:0003700; F:transcription factor erPro; IPR001005; Myb\_DNA\_binding.m; PF00249; myb\_DNA-binding; 3.

activity;

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Genew; HGNC GK; P10244;

HGNC:7548; MYBL2

TRANSFAC;

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RA Strausberg R.D., Felingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschenko L., Marusina K., Farmer A.A., Rabin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
RA Richards S., Worley A.C., Shevchenko Y., Bouffard G.G.,
RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Thuman and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bartsch O., Horstmann S., Toprak K., Klempnauer K.H., F
"Identification of cyclin A/Cdk2 phosphorylation sites
Eur. J. Biochem. 260:384-391(1999).
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION OF THR-440; THR-444; THR-494; THR-520 MEDLINE=99195476; PubMed=10095772;
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EMBL; BC007585; AAH07585.1;
PIR; S01991; S01991.
HSSP; Q03237; 1A5J.
                                                                                                            EMBL; X13293; CAA31655.1; EMBL; AL121886; CAC08392.
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yclin A/Cdk2 at sites that enhance its transactivation
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                                                                                                                                                                                                                                                              requires a license agreement
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; CAC08392.1; -.
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DNA_BIND 26
DNA_BIND 130
DNA_BIND 130
MOD_RES 444
MOD_RES 449
MOD_RES 494
MOD_RES 494
MOD_RES 577
                                                                                                                                                 MEDLINE=93049214; PubMed=1425593; Foos G., Grimm S., Klempnauer K.-H.; Foos G., Grimm S., Klempnauer K.-H.; "Functional antagonism between members inhibits v-myb-induced gene activation. EMBO J. 11:4619-4629(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHICK
            MEDLINE=98322063; PubMed=9657674; McIntosh P.B., Frenkiel T.A., Wollborn U., McKlempnauer K.H., Feeney J., Carr M.D.; "Solution structure of the B-Myb DNA-binding d for conformational instability of the protein control of gene expression."; Biochemistry 37:9619-9629(1998).
                                                                                                                         STRUCTURE BY NMR OF 79-186
                                                                                                                                                                                                                                                                                            Archosauria;
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                           Myb-related protein MYBL2 OR BMYB.
                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1993
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PS00037; MYB_1;
PS00334; MYB_2;
PS50090; MYB_3;
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(Rel. 27,
(Rel. 41,
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Aves; Neognathae; Galliformes; Phasianidae;
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V-MYB- AND C-MYB-MEDIATED ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
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No. 8.
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                                                                                          McCormick J.E.,
                                           domain:
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                                          a possible binding and
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RESULT 15
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MYB DROME 904197; Q9VXM9; 20-MAR-1987 (Re) 16-OCT-2001 (Re) 16-OCT-2001 (Re)
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PROSITE; PS00037; MYB 1; 3.

PROSITE; PS00334; MYB 2; 3.

PROSITE; PS50090; MYB 3; 3.
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TRANSFAC; T01586; -.
InterPro; IPR001005; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
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between the Swiss Institute of Bioinformatics and the EMBL
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TISSUE SPECIFICITY: EXPRESSED IN HEMATOPOIETIC HEMATOPOIETIC CELLS.
SIMILARITY: Contains 3 Myb-like domains.
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 sequence update) annotation updat
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Pred. No. 2.
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 update)
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BER OF THE MYB FAMILY.
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RX MEDLINEE2019606; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Frandell M.D., Zhang Q., Chen L.X.,
RA Baradon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bartis K.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gherry J.M., Cawley S., Dahlke C., Davenpoort L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpoort L.B., Davies P.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Guzen C., Ferriara S., Pleischhann W.,
RA Glodek A., Gong F., Gorrell J.H., Guzen B., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Guzen B., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,
RA Melnert K., Renington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Sunger D.R., Scheeler F., Shen H.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden K., Melson D.L., Weinstcok G.M., Weissenbach J.,
RA Shue B.C., Siden K., Rubin G.M., Zhou S., Zhu X., Smith H.O.,
RA Shue B.C., Shen B., Ra Weinstock G.M., Weissenbach J.,
RA Shue B., Shen B., Ra Weinstock G.M., Weissenbach J.,
RA Shue B., Shen B., Ra Weinstock G.M., Weissenbach J.,
RA Shen B., Shen B
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Beoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                   Watzen A.L., Kornberg .... "Isolation of the proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-441 FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Oregon-R;
MEDLINE=88082681; PubMed=3121304;
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SEQUENCE 5'-YAAC(G/T)G-3'.

SEQUENCE 5'-YAAC(G/T)ON: Nuclear.
                                                                                         s SWISS-PROT entry is copyright. It is produ
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287:2185-2195(2000).
                           pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                           Kornberg T.B., Bishop J.M.; f the proto-oncogene c-myb from
agreement
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Noved. Usage by and for commercial (See http://www.isb-sib.ch/announce.
                                                                                                                               is produced through a collaboration - ormatics and the EMBL outstation -
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share two conserv
domain.";
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InterPro; IPR00105; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 3.
SMART; SM00717; SANT; 3.
SROSITE; PS00037; MYB 1; 3.
PROSITE; PS00034; MYB 2; 3.
PROSITE; PS00034; MYB 3; 3.
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DNA_BIND
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EMBL; M11281; AAA70367.1;
PIR; S00578; TVFFMA.
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                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                GO: 0008283; P:cell proliferation;
251
                     133
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                                                                                                                                            l Similarity
57; Conserv
                     I-STKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDAS
LKSSRTHLITLIKSGGISKCMNNMQHN-----
                                                                    EVDLILRLHKLLGNRWSLIAGRLÞGRTANDVKNYWNTNLLRKLNTTKIVÞREKINNKCGE
                                                                                             KGPWTRDEDDMVIKLVRNFGPKKWTLI-ARYLNGRIGKQCRERWHNHLNPNIKKTAWTEK
                                                                                                                    KGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQD
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657 AA;
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MYB 2.
MYB 3.
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QL -> KY (IN REF. 3
                                                                                                                                                                                            8265B37ABB250AE4 CRC64;
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Search Job tim rch completed: January time : 20 secs 29, 2004, 20:11:54

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1477
1 MNSTSMSSLGVRKGSWTDEE.....QQGVQNDDFSAEIDLWNLLD 274
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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34.1	35.5	36.1	36.2	36.3	36.5	36.6	36.6	36.7	36.8	37.0	37.3	37.6	46.2	46.6	47.0		Ouerv
139	212	249	248	120	307	129	250	246	247	127	129	127	255	255	. 255	Length	
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Q9fnv8 arabidopsis	_	Q9ztc3 arabidopsis	Q9fe25 arabidopsis		•				vitis la	Ξ.	٣.	Q9m717 petunia hyb		Q9m720 petunia int	Q9m721 petunia hyb	Description	

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395.5	396	396	396	396	397	397.	397	397	397	399.5	399.5	400	401	402.5	402.5	403	403	403	403	404	405.5	408	409	415	423.5	428	433	438.5
26.8	26.8		26.8	•	26.9	26.9	26.9	٠	26.9	27.0			27.1	•		27.3		27.3		27.4			•	28.	28.	29.	29.3	29.
184	264	198	181	113	342	271	271	267	266	264	193	193	203	226	226	257	246	226	218	264	388	269	272	302	249	254	247	1/7
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Q94fg5	Q9atd1	049017	Q8h262	Q93v39	Q9£j07	Q8grw4	Q41842	022450	Q41868	Q9xiu9	Q94fg3	049018	Q9sei0	Q8h256	049021	Q989k9	Q9s7y2	Q8h255	Q8h253	Q41869	Q40920	Q42379	Q9zr50	Q9atd5	Q38850	Q9atd2	Q9atd9	Qyacas
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# ALIGNMENTS

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Query Match 47.0%; Score 694.5; DB 10; Length 255; Best Local Similarity 53.7%; Pred. No. 6.2e-47;	SEQUENCE 255 AA; 29021 MW; 3C590E8473209A52 CRC64;	ing; Nuclear protein.	PROSITE; PS50090; MYB_3; 2.	PS00334; MYB_2;	PROSITE; PS00037; MYB 1; 1.	SMART; SM00717; SANT; 2.	Pfam; PF00249; myb DNA-bInding; 2.	InterPro; IPR001005; Myb DNA binding.			L; AF146702; AAF66727.1;	-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		color.";	lar analysis	R.,	Quattrocchio F., Wing J., van der Woude K., Souer E., de Vetten N.,		STRAIN=cv. V26; TISSUE=Petal limb;	SEQUENCE FROM N.A.	E	=4102;	; Solanaceae; Petunia	edons; core el		Petunia hybrida (Petunia).	AN2.	•	(TrEMBLrel. 23, Last annotation	(TrEMBLrel. 15,	01-OCT-2000 (TrEMBLrel. 15, Created)	•	Q9M721 PRELIMINARY; PRT; 255 AA.	7721 .	ULT 1	

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Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
SMOSITE; PS00037; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear Protein.
SEQUENCE 255 AA; 29007 MW; 48B18508
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01-OCT-2000
01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Cell 11:1433-1444(1999).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.

EMBL; AP146703; AAF66728.1; -.

HSSP; P06876; 1MBK.
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AN2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. S9; TISSUE=Petal limb;
MEDLINE=99380006; PubMed=10449578;
Quattrocchio F., Wing J., van der Woude K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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VP---REKINNKCGEISTKIEIIKPQRRKYFSSTMKNVT-----
                                                                      RPHIKGGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLRKKL----I
                                                                                              RPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKI
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Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00717; SANT; 2.
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MEDLINE=99380006; PubMed=10449578;
Quattrocchio F., Wing J., van der Woude K.,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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PROSITE; PS0090; MYB 3; 2.
DNA-Binding; Nuclear protein.
SEQUENCE 255 AA; 28963 MW;
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06; PubMed=10449578;
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PROSITE; PS00037; MYB 1; 1.

PROSITE; PS00334; MYB 2; 1.

PROSITE; PS50090; MYB 3; 2.

DNA-binding; Nuclear protein.

SEQUENCE 127 AA; 14789 MW;
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Q9M718;
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SEQUENCE FROM N.A.
STRAIN=cv. W22; TISSUE=Petal limb;
STRAIN=q9380006; PubMcd=10449578;
Quattrocchio F., Wing J., v Mol J., Koes R.; "Molecular analysis of the in the evolution of flower
                                                                                                                SEQUENCE FROM N.A.
STRAIN-cv. W115; TISSUE-Petal limb;
MEDLINE-99380006; PubMed=10449578;
                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyt; Spermatophyta; Magnoliophyta; eudicotyledons; core Asteridae; lamiids; Solanales; Solanaceae; Petunia
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-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF146706; AAF66731.1; -.
HSSP; P06876; IMBK.
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Spermatophyta; Magnoliophyta; 6
Asteridae; lamiids; Solanales;
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Pfam; PF00249; myb DNA-binding; 2.
SMART; SMO0717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 129 AA; 15084 MW; 12D9DD38
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Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00717; SANT; 5.
PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                               Quattrocchio F., Wing J., van der Woude Mol J., Koes R., "Molecular analysis of the anthocyanin2 in the evolution of flower color."; Plant Cell 11:1433-1444(1999).
                                                                                         DNA-binding; Nuclear protein. SEQUENCE 127 AA; 14817 MW;
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-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF146707; AAF66732.1; -.
HSSP; P06876; 1MBK.
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Spermatophyta; Magnoliophyta; eudicotyledons; core
Asteridae; lamiids; Solanales; Solanaceae; Petunia
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STRAIN=Cv. W44; TJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSTSNASTSGVRKGAWTEEEDLLLRECIEKYGEGKWHLVPVRAGLNRCRKSCRLRWLNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.3%;
79.2%;
                       37.0%;
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15,
23,
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15;
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  Score 547; DB
Pred. No. 1.1e
L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 551; DB 10;
Pred. No. 5.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12D9DD38441D2427 CRC64;
                                                                                           F928569624274F35 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAINS
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DB 10;
l.1e-35;
hes 8;
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edons; core eudicots;
                                                 DB
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                                          Length
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    Indels
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  4.
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  Gaps
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MNSTSMSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYL

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RESULT 8
Q9FNV9
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OR 15P2

ID 25P2

ID 700

OR 000

OR 0
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Best Local Similarity
Matches 121; Conserv
Q9FNV9
Q9FNV9;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8L5P2;
Q8L5P2;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vitis labrusca x Vitis vinifera.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myb-related VLMYBA1-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SMOU717; SANT; 2.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 247 AA; 28255 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001005; Myb_DNA_binding.
Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=105599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMDNV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPREK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKI 120
                                                                                                                                                                                                                                                                                                     GEFSLNLPPMQQGVQNDDFSAEIDLWN
                                                                                                                                                                                                                                                                                                                                                                                                                           D-PWWINLLENCHDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQISHENW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MESLGVRKGAWIQEEDVLLRKCIEKYGEGKWHLVPLRAGLNRCRKSCRLRWLNYLKPDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSSIGVRKGSWTDEEDFILRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGEFALDEVDLMIRLHNLLGNRWSLIAGRLPGRTANDVKNYWHGHHLKK----KVQFQEE 116
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                                                                                                                                                                                                                                                GB-
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
transcription factor VINYBA1-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
(TrEMBLrel. (TrEMBLrel.
                                                                                          PRELIMINARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.8%;
45.3%;
                                                                                                                                                                                                                                                                                                                                                                -ELDQETDFSASGEMLIASLRAEETAT--
16,
                                                                                                                                                                                                                                                GDFPFDVGFWD
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Created)
Last seq
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Pred. No. 4.6e-35;
5; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9AA1717840F8A88D CRC64;
sequence update)
                                                                                                                                                                                                                                                                                                        271
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                                                                                          246
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                                                                                                                                                                                                                                                                                                                                                                   -QKKGPMDGMIEQIQG
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      RESULT
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Kim C.J., Koo H.L., Kremenetekaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetekaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetekaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear Procein.
SEQUENCE 246 AA; 28307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stracke R., Weisshaar B.; "MYB transcription factor gene nomenclature in Arabidopsis thaliana."; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative transcription factor MYB113 (Myb-related transcription factor, putative).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001005; Myb_DNA_binding Pfam; PF00249; myb_DNA-binding; 2. SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana."
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                                                                                             183
                                                                                                                                                        168
                                                                                                                                                                                                                123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               67
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                                                                                                                                                                                                                                                                                                                                 SPKGLRKGTWTTEEDILLRQCIDKYGEGKWHRVPLRTGLNRCRKSCRLRWLNYLKPSIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSIGVRKGSWTDEEDFILRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
                                                                                             CNKDEQKDKLININLLDGDNMWWESLLE
                                                                                                                                                  C-KEIISEKOTPDASMDNVDPWWINLLE
                                                                                                                                                                                                                NKNITSHPTSSAQKIDVLKPRPRSFSDKNSCNDVNILPKVDVVPLHLGLNNNYVCESSIT
                                                                                                                                                                                                                                                                         REKINNKCGEISTKIEIIKPQRRKYFSSTMKNVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 542.5; DB 10
Pred. No. 5.5e-35;
6; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FF1C4B9176040D20 CRC64;
                                                                                                                                                           194
                                                                                                210
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FOR THE PROPERTY OF STATE OF S
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I "A myb-related gene of the Kyoho grape (Vitis labruscana) reg

I anthocyanin biosynthesis in grapes.;

L Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.

R EMBL; AB073010; BAC07537.1; --

R InterPro; IPR001005; Myb DNA binding.

R Pfam; PF00249; myb DNA-binding; 2.

R Pfam; PF00249; myb DNA-binding; 2.

R PROSTIEE; PS50090; MYB 3.

DNA-binding; Nuclear protein.

DNA-binding; Nuclear protein.
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Best Local Similarity
Matches 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9M715;
01-OCT-2000
01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8L5P3;
SEQUENCE FROM N.A.
STRAIN=cv. S1; TISSUE=Petal
MEDLINE=99380006; PubMed=10
                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitis labrusca x Vitis vinifera.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9M715
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                                                                                                                                              NCBI_TaxID=33119;
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                                                                                                                                                                                                                                                                                                                                                                                 protein.
           PubMed=10449578;
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Last sequence update)
Last annotation updat
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Pred. No. 7.4e-35;
7; Mismatches 82; Indels
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                                                     Query Match
Best Local S
Matches 124
                                                                                                                                           STRAIN-CV. Kyoho; TISSUE-Fruit;

R Kobayashi S., Ishimaru M., Hiraoka K., Honda C.;

R Kobayashi S., Ishimaru M., Hiraoka K., Honda C.;

R M myb-related gene of the Kyoho grape (Vitis labruscana) r

I anthocyanin biosynthesis in grapes.";

I submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

C-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

C-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.

R EMBL; AB073013; BAC07540.1; --

R InterPro; IPR001005; Myb DNA_binding.

R Pfam; PF00249; myb DNA_binding; 2.

R SMART; SM00717; SANT; 2.

R SMART; SM00717; SANT; 2.
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Pfam; PF00249; myb_DNA-binding; 2.
SMART; SMO0717; SANT; 2.
PROSITE; P500037; MYB 1; 1.
PROSITE; P5000334; MYB 2; 1.
PROSITE; P5000349; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 129 AA; 15041 MW; 0E3731FD
                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myb-related transcription factor VlMYBA2.
VLMYBA2.
                                                                                                                                                                                                                                                                                                                                                           VIMXHAZ.
VITIS labrusca x Vitis vinifera.
Eukaryota; Viridiplantae; Streptophyta; Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular analysis of the anthocyanin2 gene of pel in the evolution of flower color."; Plant Cell 11:1433-1444(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF146708; AAF66733.1; --
HSSP; P06876; 1MBK.
                                                                                                          PROSITE; PS50090; MYB_3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 307 AA; 34891 MW;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quattrocchio F., Wing J., van der Woude
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=105599;
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                                                      124;
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                         σ
                                                                  Similarity
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             MSSIGVRKGSWTDEEDFILRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIK
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MESIGVRKGAWIQEEDVLLRKCIEKYGEGKWHLVPLRAGLNRCRKSCRLRWLNYLKPDIK
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                                                      Conservative
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                                                   36.5%; Score 539.5; DB 1
46.6%; Pred. No. 1.2e-34;
tive 35; Mismatches 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 540;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0E3731FDD84FD1C7 CRC64;
                                                                                                            682ACD258C3007BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4e-35;
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                                                                                                                                                                                                                                                                                                                                                                                 Embryophyta; Tracheophyta;
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                                                                                DB 10;
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                                                      88;
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s labruscana)
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                                                                                                                                                                                                                                                                                                                                                                    core eudicots; Vitaceae;
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Best Local :
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SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS00304; MYB 3; 2.
DNA-binding; Nuclear protein.
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Q9M714;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular analysis of the anthocyanin2 in the evolution of flower color."; plant Cell 11:1433-1444 (1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SI--!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMA EMBL; AF146709; AAF66734.1; -.
HSSP; P06876; 1MBK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. 57; TISSUE-Petal limb;
MEDLINE-99380006; PubMed=10449578;
Quattrocchio F., Wing J., van der Woude
Mol J., Koes R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                     DNA-binding; No SEQUENCE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=33119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petunia axillaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001005; Myb_DNA_binding.
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APHD
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79.0%;
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Last annotation update)
                                                                                                                                                                                                                                                         Score 536; DB
Pred. No. 7.5e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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1. No. 7.5e-35;
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RESULT 13 Q9FE25

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Q9FE25;
01-MAR-2001
01-MAR-2001
01-MAR-2003
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-cv. Columbia-0;
Borevitz J.O., Xia Y., Blount J.,
"Activation Tagging Identifies a '
Phenylpropanoid Biosynthesis.";
Plant Cell 12:0-0(2000).
                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear Protein.
SEQUENCE 248 AA; 28469 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of anthocyanin
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EMBL; AC009323; AAG09100.1; -.
HSSP; P06876; 1IDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                             KMKKRDITPIPTTPALKNNVYKPRPRSF-----TVNN
                                                                                                                                                                   GKLSSDEVDLLLRLHRLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHE
                                                                                                                                                                                     GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKI
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LEES-QEVDILVPEATTTEKGDTLAFDVDQLWSLFD
                       SHENWGEFSLNLPPMQQGVQNDDFSAEID-LWNLLD
                                                                                ASMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQI
                                                                                                                                                                                                                           SSKGLRKGAWITTEEDSILRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR
                                                    ----DVNPPCLGL--NINNVC--DNSIIYNKDKKKDQLVN--
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(TIEMBLrel. 16, Last sequence update)
(TIEMBLEL 23, Last amnotation update)
of anthocyanin pigment 1 protein (Putative transcription
                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 2.2e-34;
0; Mismatches 68;
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                                                                                                                                                                                                                                                                                    68;
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3 Regulator
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Buehler E., Chin
Kim C., Koo T.,
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Toriumi M.,
Toriumi R.W.;
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With Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

AN White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

AN Chan E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

With Chan E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chan B., Connay A.B., Conway A.R., Creasy T.H., Dewar K.,

AN Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

AN Chung M.K., Conn L., Conway A.B., Conway J. R., Fujii C.Y.,

AN Chung M.K., Conn L., Conway A.B., Conway J., Fong B., Fujii C.Y.,

AN Chung M.K., Condsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

AN Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

AN Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B.,

A Kim C.J., Koo H.L., Kremenetskaia V.S., Walker M.,

Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis

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"" "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                 Query Match
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Matches 122
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Putative tra
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Borevitz J.O., Xia Y., Blount J., Dixon R.A., I
"Activation Tagging Identifies a Conserved MYB
Phenylpropanoid Biosynthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petroni K., Urzainqui A., Bevan M., Martin (Tonelli C., Paz-Ares J., Weisshaar B., "Towards functional characterisation of the gene family from Arabidopsis thaliana.", Plant J. 16:263-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYB90 OR PAP2 OR T27F4.14.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                              PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001005; Myb DNA binding. Pfam; PF00249; myb DNA-binding; 2. SMART; SM00711; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC020665; AAG
HSSP; P06876; 1IDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILA-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS. EMBL; AF062915; AAC83637.1; -. EMBL; AF325124; AAG42002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein) (MYB-related
67047).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence and thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                                                                                                                           DNA-binding; Nuclear
SEQUENCE 249 AA; :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H.D.,
                                                                                                                                                Similarity
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v. Columbia;
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003 (TrEMBLrel. 23, Last annotation update)
transcription factor (Production of anthocyanin pigment
(MYB-related transcription factor, putative, 65699-
                               SSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKR
SSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKR
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Urzainqui A., Bevan M., Martin C.,
                                                                                                                    Conservative
                                                                                                                                                                                                                                        ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG52164.1; -.
                                                                                                                                                                                                                                        28100 MW;
                                                                                                                                                36.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEAR (BY SIMILARITY).
                                                                                                 Score 532.5; ; Pred. No. 3.4e: 34; Mismatches
                                                                                                                    34;
                                                                                                                                                                                                                                           309024FD4103700A CRC64;
                                                                                                       e 532.5; Db ...
1. No. 3.4e-34;
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Smeekens
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S.,
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                                                                                                                                                                             249;
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RESULT
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Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Wagnoliophyta; eudicotyledons; core eudicots; Rosid
Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00034; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein
SEQUENCE 212 AA; 24508 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P06876; 1IDY.
InterPo; IPRO01005; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLANT J. 18:285-2/6(1895).
-i- SUBCELIULAR LOCATION: NUCLEAR (BY SIMILARITY)
-i- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL, AF082908; AAC83630.1; -.
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01-MAR-2003
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VILDEEHCKEIISEKQTPDASMDNVDPWWI
                                                                                                                                                                                                    GDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRK-------
                                                                                                                                                                                                                                                                    SSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKR
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                                                                         DITPIPTTPALKUNVYKPRPRSFTVNNDCNHLNAPPKVDVNPP-
                                                                                                                                                                         GKLSSDEVDLLLRLHRLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKIKMKKR
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                                                                                                                                                                                                                                                                                                                                                                                     35.5%;
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Pred. No. 1.3e-33;
3; Mismatches 38;
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1 C., Smeeke
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                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Db 180 IIYNKDKKKDQLVN------NLIDGDNMWL 203
Search completed: January 29, 2004, 20:12:48
Job time: 43 secs

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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6 2.2 371 21 AAG236530 Arabidops: 6 2.2 371 21 AAG226530 Arabidops: 6 2.2 371 21 AAG236530 Arabidops: 6 2.2 372 21 AAG23758 Arabidops: 6 2.2 372 21 AAG3333 Arabidops: 6 2.2 373 21 AAG30101 Arabidops: 6 2.2 374 22 AAB99728 Helicobact 6 2.2 374 23 ABU51613 Helicobact 6 2.2 375 22 AAB01744 M. tubercu 6 2.2 376 19 AAW64377 Mycobactes	6 2.2 365 24 6 2.2 369 21 6 2.2 370 21	6 2.2 355 21 AAG28148 6 2.2 356 23 AAO22175 6 2.2 356 23 ABB55105 6 2.2 357 22 AAU45695 6 2.2 357 22 AAU48095 6 2.2 357 23 ABB55078 6 2.2 361 23 ABB55078 6 2.2 362 23 AAU80013 6 2.2 362 23 AAU79807 6 2.2 363 20 AAY37863 6 2.2 365 23 ABB48295	6 2.2 341 24 ABU07760 6 2.2 342 21 AAG41495 6 2.2 342 21 AAG41495 6 2.2 347 23 ABP41961 6 2.2 347 18 AAW20595 6 2.2 348 22 AAM41060 6 2.2 350 21 AAG214334 6 2.2 350 21 AAG277189 6 2.2 350 22 ABG27189 6 2.2 351 22 AAM79201 6 2.2 351 23 ABB92633 6 2.2 351 23 ABB92633 6 2.2 352 18 AAW30300 6 2.2 353 21 AAG36439 6 2.2 353 21 AAG36439	6 2.2 330 21 AABC0354 6 2.2 329 24 ABP76728 6 2.2 329 24 ABP76728 6 2.2 329 24 ABP76728 6 2.2 330 21 AAG58896 6 2.2 330 21 AAG58896 6 2.2 330 22 AAB60354 6 2.2 330 22 AAB60354 6 2.2 330 22 AAB60370 6 2.2 335 23 ABB92283 6 2.2 335 24 ABP81239 6 2.2 336 22 AAB60370 6 2.2 336 22 AAB79137 6 2.2 336 22 AAB79137 6 2.2 336 22 AAB79487 6 2.2 336 23 ABP69364 7 23 341 23 ABP69274 8 Tryy 8 C2 341 23 ABP26965 8 2.2 341 23 ABP26965 8 2.2 341 23 ABP26965 8 C2 341 23 ABP26965	6 2.2 318 23 AAU95699 6 2.2 318 24 ABU11220 6 2.2 319 21 AAG55058 6 2.2 319 23 AAU76435 6 2.2 320 21 AAG60193 6 2.2 321 21 AAG34413 6 2.2 322 21 AAB25329 6 2.2 323 21 AAG82096 6 2.2 324 22 AAG82096 6 2.2 324 22 AAG82096 6 2.2 327 22 AAG82097

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RESULT 1:
ABB81626
ID ABB8
XX ABB8
XX ABB8
XX ABB8
XX Toma
XX Toma
XX Toma
XX Toma
XX Hycc
PN WO20
XX Lycc
PN WO20
XX ABB8
XX Toma
XX 
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                                                                                                                                29-OCT-2001; 2001WO-US50638
                                                                                                                                                                     18-JUL-2002.
                                                                                                                                                                                                                                            Lycopersicon esculentum.
                                                                                                                                                                                                                                                                              Tomato; ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour
                                                                                                                                                                                                                                                                                                                     Tomato anthocyanin 1 (ANT1) protein SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                         24-SEP-2002 (first entry)
                                                                                                                                                                                                         WO200255658-A2
                                                                                                                                                                                                                                                                                                                                                                                              ABB81626;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB81626 standard; Protein; 274 AA
                                                         (EXEL-) EXELIXIS PLANT SCI INC.
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                                                                                              2000US-2446B5P.
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376
376
378
379
                     Liu A;
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AAY39723
AAG33722
AAG63553
AAG46567
AAM581539
ABG05463
AAG61539
ABG05463
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AAF62003
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AAF62003
AAG61007
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AAG81305
AAG44396
AAY68793
AAY78638
AAY78638
AAY78638
AABG07531
ABG1259
AAB004473
AAB04473
AAB04614
AAU01868
AAU00267
AAB062890
AAB062890
AAB062890
AAB06251
AAAG34075
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ABP41651
AAG25463
AAG26529
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Abscisic acid resp
Arabidopsis thalia
C glutamicum prote
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Arabidopsis thalia
Protein regulating
Novel human diagno
Novel human diagno
Novel human diagno
Arabidopsis thalia
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Sequence encoded b
Mycobacterium tube
Novel human diagno
Human ovarian anti
Arabidopsis thalia
Arabidopsis thalia
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Arabidopsis thalia
Arabidopsis thalia
Helicobacter pylor
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Staphylococcus epi
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Human AFP protein
Arabidopsis thalia
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Arabidopsis thalia
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polypeptide,
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RESULT 2
AAE01933
ID AAE01933
ID AAE01933
ID AAE0
XX AAE0
XX AAE0
XX Tran
KW Tran
KW Stru
KW agri
XX Arah
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Best Local S
Matches 274
                   17-NOV-1999;
17-APR-2000;
22-AUG-2000;
                                                                                                                                25-MAY-2001
                                                                                                                                                                     WO200135727-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE01933;
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N-PSDB; ABQ73046.
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The present sequence represents tomato anthocyanin 1 (ANT1). The ANT1 polynucleotide can be used for modifying the expression of a native plant gene, particularly for producing an anthocyanin 1 phenotype in plants, which is responsible for many red and blue colours in plants. The polynucleotide is useful for modifying e.g. leaf colour, flower colour or fruit colour in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide derived from tomato, useful for producing an Anthocyanin 1 phenotype in plants, particularly for modifying e.g. leaf color, flower color or fruit color in plants
                                                                                              14-NOV-2000; 2000WO-US31457
                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                          agricultural biotechnology.
                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor; trait modification; seed characteristic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana transcription factor homologue G2421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE01933 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 39-41; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPREKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKI
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; 99US-0166228.
; 2000US-0197899.
; 2000US-0227439.
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                                                                                                                                                                                                                                   /label= Conserved_domain
                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
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Pred. No. 2.4e-262;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
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RESULT 3
AAU93176
ID AAU9
XX AAU9
XX AAU9
XX AAU9
XX Arab
XX Arab
XX Micri
KW Micri
KW Micri
KW Plar
XX Plar
XX Plar
OS Arab
XX WO2(
XX WO2(
XX 28-1
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PR 22-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characteristics of plants, e.g., corn, potato and cotton plants, when their expression level is altered. Specifically, they are used for modifying the nutritional content of plants or seeds, e.g., to modify vitamin and mineral content, to modify the oil content of seeds, to modify the insoluble sugar content of seeds, to modify the plants or seeds, to modify the insoluble sugar content of seeds, to modify plants and modify wax content. They may also be used to alter seed characteristics such as shelf-life, size, stress colerance, seedling vigour, pest and pathogen resistance and germination rate. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reuber L,
Pineda O,
                                                                                                                                                          plant; transcription factor;
                                                                                                                                                                       Agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                                                                                                                                                                                                  02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor G663. The transcription factors may be used to modify traits associated with structural or developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding plant transcription factor polypeptides, for altering the developmental and structural characteristics o plants, e.g. corn, potato and cotton plants -
22-AUG-2000; 2000US-227439P.
16-NOV-2000; 2000US-0713994.
                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                  Arabidopsis transcription factor #214.
                                                                                                                                                                                                                                                                                                                           AAU93176 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 116; 133pp; English
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                                          22-AUG-2001; 2001WO-US26189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                               78 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
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JIANG C.
YU G.
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REUBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                   LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Creelman R,
Heard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is homologue G2421 of Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                            transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang
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RESULT 4 AAE01932

standard;

Protein;

246

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31-JUL-2001 AAE01932; AAE01932

(first entry)

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                                                               Query Match
Best Local S
Matches 32
                                                                                                                                                                                  recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant or the plant exhibits ectopic expression or altered expression or altered expression or altered expression.
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a
                                                                                                                                                                                                                                                                                                                                                                                                homologue sequence from a database comprising a plurality of known plant
sequences comprising inputting sequence information selected from one of
464 fully defined sequences given in the specification. The isolated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 40;
                                                                                                                                                                      A. thaliana transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An isolated or recombinant polynucleotide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABK65362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pilgrim M, Creelman R, Dubell I
Adam L, Ratcliff O, Reuber JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-2001; 2001US-0837944.
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JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEDDIE J.
ADAM L.
                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DUBELL A J.
                   LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
LRIHKILGNRWSLIAGRIPGRTANDVKNYWNT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 878-879; 941pp; English.
                                                                                                                                       209 AA;
                                                               Conservative 0;
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                                                                               Score 32;
Pred. No.
                                                                  Mismatches
                                                                 3.3e-23;
hes 0;
                                                                                                   DB 23;
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                                                                                                 Length 209;
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                                                                  Indels
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RESULT 5
AAU93177
ID AAU9
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                                                                                                                                   Query Match
Best Local
                                                                                                                       Matches
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AAU93177 standard; Protein; 246 AA
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Pineda
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(PILG/)
(RIEC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1999; 99US-0166228.
17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                 plants, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding plant transcription factor polypeptides, useful for altering the developmental and structural characteristics of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana transcription factor homologue G2422.
                                                                                                                                                                         Sequence
                                                                                                                                                                                                     agricultural biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-335979/35.
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                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                        4; Page 114; 133pp;
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RIECHMANN J L.
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CREELMAN R.
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REUBER L.
                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PINEDA O.
                                                                 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 106
                                                                                            LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Creelman | Heard J;
                                                                                                                                                                         246 AA;
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 9..110
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                                                                                                              11.7%; 5c.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                              pest and pathogen resistance and germination d in gene therapy. Therefore manipulating s in plants offers great potential in for modifying a plant's traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t modification;
developmental c
                                                                                                                                  Score 32;
Pred. No.
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                                                                                                                       Mismatches
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                                                                                                                                                 DB 22;
                                                                                                                                3.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; seed characteristic;
characteristic; gene therapy;
                                                                                                                       0,
                                                                                                                                              Length 246
                                                                                                                       Indels
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22-AUG-2000; 2000US-227439P
16-NOV-2000; 2000US-0713994
16-APR-2001; 2001US-0837944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
                                                                                        Pilgrim
                                                                                                                                                                                                                                                        (CREE/)
                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2001; 2001WO-US26189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant; transcription factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis transcription factor #215.
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(RATC/)
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                                                                                                                                                                    (REUB/)
                                                                                                                                                                                                                (KEDD/)
isolated or recombinant polynucleotide
                                              2002-292022/33
                                                                                                                                                                 CREELMAN R.
DUBELL A J.
HEARD J.
JIANG C.
KEDDIE J.
ADAM L.
RATCLIFF O.
REUBER J L.
                                                                                        3
                                                                                                                       PINEDA O
                                                                                                                                                   REUBER J L.
RIECHMANN J
                                                                                                                                                                                                                                                                                                     MENDEL BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                                       PILGRIM M.

    Creelman
Ratcliff O,

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                                                            1 R, Dunc.
Reuber JL,
                                                              Dubell AJ, Hearn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic
                                                                            Heard J,
echmann JL,
   used
                                                                            Jiang C,
L, Yu G,
   ç
 produce a transgenic
                                                                            Keddie J;
Pineda O;
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Claim 40; Page 880-881; 941pp; English

CC encoding an Arabidopsis thaliana transcription factor, their variants, CC encoding an Arabidopsis thaliana transcription factor, their variants, CC complements, fragments, or related polynucleotide with 31% to 95% CC sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered CC phenotype as compared to a wild-type or reference plant, or the plant of one or more genes CC associated with a plant trait as compared to a wild plant. Also included CC are a transgenic plant comprising the polynucleotides, a computer CC readable medium having stored sequence information, and identifying a CC homologue sequence from a database comprising a plurality of known plant CC sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or CC recombinant polynucleotide is used for producing a plant having a CC modified trait, the method comprising selecting a polynucleotide that CC encodes a polypeptide or an antisense nucleic acid, inserting the polynucleotide to a plant to a cell of a plant to overexpress CC the polypeptide or antisense nucleic acid, thereby producing a modified C production of agriculturally useful proteins or metabolic chemicals, gest tolerance, herbicide resistance, seed and fruit yield, growth contact of the co The invention relates to 1 of 232 isolated or recombinant polynucleotides

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Specifically, they are specifically, they are specifically, to plants or seeds, e.g., to plants or seeds, content of seeds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification). The present sequence is A. thaliana transcription factors.
                               The present sequence is Arabidopsis thaliana transcription factor The transcription factors may be used to modify traits associated with structural or developmental characteristics of plants, e.g., potato and cotton plants, when their expression level is altered.
                                                                                  Claim
                                                                                                     Nucleic acids encoding plant transcription factor polypeptides, for altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants -
                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                   14-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agricultural biotechnology.
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(CREE/)
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17-APR-2000;
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CREELMAN R.
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                                                                                  Page 70-71;
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                                                                                                                                                                          Creelman Heard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characteristic;
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2000US-0197899.
2000US-0227439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor; trait modification;
             they are used for modifying the nutritional content of ds, e.g., to modify vitamin and mineral content, to mod
                                                                                                                                                                                                                                                                                      BIOTECHNOLOGY INC
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                                                                                 133pp;
                                                                                                                                                                                    Pilgrim M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental
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                                                                                  English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32;
Pred. No.
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    o modify
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RESULT 7
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Best Local S
Matches 32
                                                                                The present sequence represents a plant stress tolerance-related myloblastosis (MYB) transcription factor. The specification describes AtMYB60, AtMYB764, AtMYB75 and AtMYB90. MYB polypeptides are useful fo enhancing a plant's tolerance or sensitivity to stress e.g. salt, drought, cold and heat tolerance. It is also useful for producing a transgenic plant with enhanced stress tolerance or stress sensitivity. MYB polypeptides are also useful for increasing the production of products of the phenylpropanoid biosynthesis pathway, e.g. stilbenes, flignins, salicylic acid, anthocyanins, and phenolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecules encoding plant stress tolerance-related myloblastosis transcription factors for increasing stress resia crop in a field -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as shelf-life, size, stress tolerance, seedling vigour, pest and pathogen resistance and germination ratio. They may also be used in gene therapy. Therefore manipulating transcription factor levels in plants offers great potential in agricultural biotechnology for modifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stress tolerance; myloblastosis transcription factor; heat tolerance; MYB transcription factor; AtMYB60; AtMYB764; AtMYB75; transgenic plant; phenylpropanoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB68356;
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                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Fig 4; 92pp; English
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                                                             derivatives.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BADI ) BASF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of MYB transcription factor AtMYB90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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Query Match
Best Local Similarity
Matches 32; Conserv

11.7%; So illarity 100.0%; I Conservative 0;

Score 32; Pred. No.

DB 22; 3.9e-23

Length 249;

Indels

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Mismatches

Sequence

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RESULT 8
AAU92969
ID AAU9
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The invention relates to 1 of 232 isolated or recombinant polynucleotides CC encoding an Arabidopsis thaliana transcription factor, their variants, CC complements, fragments, or related polynucleotide with 31% to 95% CC sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered CC phenotype as compared to a wild-type or reference plant, or the plant c or more genes CC associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer CC readable medium having stored sequence information, and identifying a CC homologue sequence from a database comprising a plurality of known plant CC sequences comprising inputting sequence information, and identifying a CC sequences comprising inputting sequence information. The isolated or recombinant polynucleotide is used for producing a plant having a CC modified trait, the method comprising selecting a polynucleotide that
                                                                                                                                                                                                                                                                                           WPI; 2002-292022/33
N-PSDB; ABK65155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2000; 2000US-227439P.
16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agriculture; metabolic chemical; environmental stress; microbial disease resistance; herbicide resistance; ser fruit yield; growth rate; leaf senescence; flower senes
                                                                                                                                                                                                                          Claim 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant; transcription factor; transgenic.
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                                                                                                                                                                                                                                                                  An isolated
                                                                                                                                                                                                                                                                                                                                   Adam L,
                                                                                                                                                                                                                                                                                                                                                 Pilgrim
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(HEAR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                   (REUB/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KEDD)
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RATCLIFF O.
REUBER J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEARD J.
JIANG C.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DUBELL A J.
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Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                        RIECHMANN J L.
YU G.
                                                                                                                                                                                                                                                                                                                                                                            PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILGRIM M
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                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                or recombinant polynucleotide
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                                                                                                                                                                                                                         97-98;
                                                                                                                                                                                                                                                                                                                                 R, Dubell AJ, Heard J, Reuber JL, Riechmann JL,
                                                                                                                                                                                                                         941pp; English.
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                                                                                                                                                                                                                                                                                                                                   Jiang C,
L, Yu G,
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                                                                                                                                                                                                                                                                  produce
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seed yield;
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Pineda O;
                                                                                                                                                                                                                                                                  a transgenic
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RESULT 9
AAU75735
ID 78735
AAU75735
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAP2; production of anthocyanin pigment; MYB-like transcription factor; transgenic; plant; phenylpropanoid; stress; light stress; water stress; phenylpropanoid; stress; pathogen attack; phenylprotuce stress; heavy metal stress; pathogen attack; infection; wounding; nutrient deficiency; herbivory; plant colouration;
                                                                                                                                                                                                                                                                                                    23-JUN-2000;
05-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                          21-JUN-2001; 2001WO-US19734
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                                                                                                                                                                     Borevitz J,
                                                                                                                                                                                                                            (SALK )
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                                                                                                                         2002-164443/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sensitisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                       SALK INST BIOLOGICAL ROBERTS NOBLE FOUND I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                  ABK14222.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana.
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                                                                                                                                                                                                                                                                                                  2000US-0603244.
2000US-0610185.
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                                                                                                                                                                        Xia Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Encoded by GAT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%;
                                                                                                                                                                           Lamb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
                                                                                                                                                                           S,
                                                                                                                                                                                                                            INC SAMM
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Pred. No.
                                                                                                                                                                             Dixon
                                                                                                                                                                                                                            SAMMUEL.
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New isolated PAP1 or PAP2 gene, useful for increasing pigmentation in plants, as reporter genes for analysing expression pattern of promoter of interest, and to increase flux through phenylpropanoid pathway

Claim

9; Page 28;

English.

relates to 29pp;

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RESULT 10
AAE30046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC 1. PAP1 and PĀP2 are MYB-like transcription factors that regulate the CC production of anthocyanin pigment. The nucleotide sequence of the CC invention is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The nucleotide sequence is also useful for screening for plant cell. The CA. thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour expression. The nucleotide sequence is also useful for enhancing CC expression. The nucleotide sequence is also useful for enhancing CC commulation of phenylpropanoid product in a plant. A transgenic CC plant is useful for detecting a stress condition such as light CC stress, water stress, pH stress, temperature stress, heavy metal CC stress, pathogen attack or infection, wounding, nutrient deficiency, CC herbivory, or abnormal hormone levels in a plant. PAP1 or PAP2 colouration in ornamental plants for commercial sales, and for colouration plants to stress. Introduction of PAP1 or PAP2 sensitises or lants to respond more contaction of PAP1 or PAP2 sensitises.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription factor; metabolite pathway; terpenoid; limonene synthase; alkaloid pathway gene; taxadiene synthase; biological pathway; freezing; abiotic stress; cold; drought, heat; nutrient deficiency; biotic stress; abiotic stress; cold; drought, mering; root development; TDS; LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plants to respond more quickly to a stress condition in ways that are physiologically significant, as well as in ways of ornamental significance. The present sequence represents the A. thaliana PAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana production of anthocyanin pigment (PAP) or PAP2. The genes for both PAP1 and PAP2 have been mapped to 1. PAP1 and PAP2 are MYB-like transcription factors that regul
Determining whether one of several test transcription factor polynucleotides encodes pathway TF by determining expression
                                                                                                                                                                                                                                                                                                                                                                                                                   alkaloid pathway gene; taxadiene synthase; babiotic stress; cold; drought; heat; nutrient infection; developmental pathway; flowering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE30046 standard; Protein; 249 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                              N-PSDB;
                                                                                                                                                                                                  16-MAR-2001; 2001US-0810836.
                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                     transgenic; transgenic plant.
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                                                                                                                                                                                                                                         15-MAR-2002;
                                                                                                                                                                                                                                                                                                                        WO200274917-A2
                                                                                                                                                               (MEND-) MENDEL BIOTECHNOLOGY INC
                                                                              2003-018799/01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                              AAD47497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G663 transcription factor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 32; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the nucleotide and protein sequences of novel uction of anthocyanin pigment (PAP) genes PAP1 have been mapped to chromosome
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                      (TF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathway gene promoter linked to reporter gene in a cell in presence of
                                                          10-MAY-2001
                                                                                       WO200132002-A1
                                                                                                                                 Misc-difference
                                                                                                                                                            Misc-difference
                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                           Arabidopsis
                                                                                                                                                                                                                                                                                                                       phenylpropanoid biosynthesis
                                                                                                                                                                                                                                                                                                                                  Stress tolerance; myloblastosis transcription factor; heat tolerance; MYB transcription factor; AtMYB60; AtMYB764; AtMYB75; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                 Amino
                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB68355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB68355 standard; Protein; 211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression of one or more genes in a pathway. The method is useful for determining whether a member of a pool of test transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a high-throughput method for identifying a polynucleotide which encodes a transcription factor for controlling the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                 acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRIHKLIGNRWSLIAGRIPGRTANDVKNYWNT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249
                                                                                                                                                                                                                                                                                                                                                                               sequence
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A
                                                                                                                                                                                       /note= "Gly encoded
                                                                                                                                                               180
                                                                                                                                                                                                                       90
                                                                                                                                 181
                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                   /note= "Asp encoded
                                                                                                                                               note= "His encoded by
                                                                                                                                                                                                                                                                                                                                                                                 Of MYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%;
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                                                                                                                                                                           "Asn
                                                                                                                    "Tyr
                                                                                                                                                                                                                                                                                                                                                                              transcription factor AtMYB75.
                                                                                                                  encoded
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                                                                                                                                                                             encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32;
Pred. No.
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                                                                                                                                                                                                                                   TTCGAT"
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05-NOV-1999;

99US-0163579

06-NOV-2000; 2000WO-US30503

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RESULT 12
AAU93155
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding plant myloblastosis transcription factors for a crop in a field -
                                                                                                               22-AUG-2000; 2000US-227439P.
16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
                                                                                                                                                                                                                                                   microbial disease resistance; herbicide resistance; seed yiel fruit yield; growth rate; leaf senescence; flower senescence. plant; transcription factor; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                             Arabidopsis
                                                                                                                                                                                                                                                                                                                                    02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                           AAU93155
                                                                                                                                                                                                                                                                                                                                                                                 AAU93155 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                 (HEAR/)
                                                                (MEND-)
(PILG/)
(CREE/)
                                                                                                                                                             22-AUG-2001; 2001WO-US26189.
                                                                                                                                                                                    28-FEB-2002.
                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                        Agriculture; metabolic chemical; environmental stress;
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          (ADAM/)
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                      KEDD/)
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DB; AAF85190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 LLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
KEDDIE J. .
ADAM L.
RATCLIFF O.
                                CREELMAN R.
DUBELL A J.
HEARD J.
JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                         MENDEL BIOTECHNOLOGY
                                                                              PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                        LLGNRWSLIAGRLPGRTANDVKNYWNT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
                                                                                                                                                                                                                                                                                                             transcription
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                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                                                                                                                                                                              factor #193
                                                                                                                                                                                                                                                                                                                                                                                  212
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 211;
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                                                                                                                                                                                                                                                                              se; drought;
seed yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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controlled sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 proteins which are
                                                                                                                                                                                                                                                                                                                                                                         encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated or recombinant polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pilgrim
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PINEDA O.
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Ratcliff O, Reuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REUBER J L.
RIECHMANN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 794-795; 941pp; English.
                                       transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dubell AJ, new-
                                         factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heard J,
echmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jiang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           produce
                                                             proteins which are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a transgenic
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밁 8 Query Match Best Local : Matches 83 LLGNRWSLIAGRLPGRTANDVKNYWNT 109 ||||||||||||||||||||||| 80 LLGNRWSLIAGRLPGRTANDVKNYWNT 106 Similarity 27; Conserv Conservative 9.9%; 0 Score 27; Pred. No. Mismatches DB 23, 0 Length 212; Indels , , Gaps 0

Sequence

212

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RESULT 13
AAU75734
ID AAU75
XX AAU75
XX AAU75
XX 08-MA
DT 08-MA
XX PAP1;
KW trans
KW trans
KW trans
KW trans
KW trans
XX Sires
XX Arabi
XX WO2000
                                                                                          PAP1; production of anthocyanin pigment; MYB-like transcription factor; transgenic; plant; phenylpropanoid; stress; light stress; water stress; pH stress; temperature stress; heavy metal stress; pathogen attack; infection; wounding; nutrient deficiency; herbivory; plant colouration;
                                                                                                                                                                                        A. thaliana Production of anthocyanin pigment 1 (PAP1)
                                                                                                                                                                                                                                08-MAY-2002
                                                                                                                                                                                                                                                                                                        AAU75734 standard; Protein; 248
                                                                          sensitisation;
                                                                                                                                                                                                                                (first entry)
                                                                            chromosome 1.
                                                                                                                                                                                            protein
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Arabidopsis

thaliana

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AAB82483
ID AAB8
XX
AC AAB8
AC AAB8
DT 22-F
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DE COLL
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KW GhM
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COS
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                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to the nucleotide and protein sequences of novel CC Arabidopsis thaliana production of anthocyanin pigment (PAP) genes PAP1 CC or PAP2. The genes for both PAP1 and PAP2 have been mapped to chromosome CC 1. PAP1 and PAP2 are MYB-like transcription factors that regulate the production of anthocyanin pigment. The nucleotide sequence of the crimvention is useful for screening for PAP gene expression, it is also useful for detecting promoter activity within a plant cell. The nucleotide sequence is also useful for screening for plant cell (e.g., A. thaliana) transformation. The transformed plant cells are then used to produce transgenic plants with tissue-specific altered colour expression. The nucleotide sequence is also useful for enhancing cacumulation of phenylpropanoid product in a plant. A transgenic colour tis useful for detecting a stress condition such as light colour stress, water stress, pH stress, temperature stress, heavy metal stress, pathogen attack or infection, wounding, nutrient deficiency, charters, pathogen attack or infection, wounding, nutrient deficiency, colouration in ornamental plants for commercial sales, and for colouration in ornamental plants for commercial sales, and for colouration plants to stress. Introduction of PAP1 or PAP2 sensitises colouration in a part of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plants to respond more quickly to a stress condition in ways that are physiologically significant, as well as in ways of ornamental significance. The present sequence represents the A. thaliana PAP1 protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated PAP1 or PAP2 gene, useful for increasing pigmentation plants, as reporter genes for analysing expression pattern of promo of interest, and to increase flux through phenylpropanoid pathway
                                                                                                                                                         Cotton transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borevitz J, Xia Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-2000;
05-JUL-2000;
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                       WO200140250-A1
                                                                  Gossypium hirsutum
                                                                                                                                                                                                      22-AUG-2001
                                                                                                                                                                                                                                                   AAB82483;
                                                                                                                                                                                                                                                                                                AAB82483 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Page 26-27; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                08
                                                                                                                                                                                                                                                                                                                                                                                                                                       83 LLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 27; Conserv
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ROBERTS NOBLE FOUND INC SAMMUEL.
                                                                                                               MYB;
                                                                                                                                                                                                                                                                                                                                                                                                                LLGNRWSLIAGRLPGRTANDVKNYWNT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 AA;
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2000US-0610185.
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                                                                                                                                                                                                      (first entry)
                                                                                                            cotton; transcription factor; transgenic plant.
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                                                                                                                                                         factor GhMYB
                                                                    Acala SJ-2
                                                                                                                                                                                                                                                                                                302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 23;
Pred. No. 3.4e-1
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thes 0;
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription in a plant involves introducing into the plant a recombinant expression cassette comprising a promoter that is operably linked to a heterologous polynucleotide encoding a MYB protein, especially GhMYB 1 or GhMYB 6. The plant is especially a cotton plant, and the promoter directs expression of the polynucleotide in cotton fibres or roots. Valuable phenotypes can be conferred on the plant by this method, e.g. increased fibre quality, yield, length, strength or fineness, alteration of root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating transcription in plants for improving cotton fiber quality, comprises introducing a recombinant expression cassette comprising a promoter operably linked to a sequence encoding a MYB polypeptide -
                                                                                                                                                                                                                 Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-2001
                                                        11-MAR-1999;
                                                                                      09-MAR-2000; 2000WO-US06112
                                                                                                                                           WO200053724-A2.
                                                                                                                                                                         Eucalyptus grandis.
                                                                                                                                                                                                                                                                                       Eucalyptus grandis transcription factor protein sequence #423
                                                                                                                                                                                                                                                                                                                     25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                  AAB33327;
                                                                                                                                                                                                                                                                                                                                                                              AAB33327 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              architecture, and enhanced growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pre-anthesis fibre cDNA library. A claimed method of modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor GhMYB 7. The sequence was deduced from GhMYB 7 c isolated from a Gossypium hirsutum cv. Acala SJ-2 10-day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of cotton R2R3-MYB transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF90596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1999;
                                            18-AUG-1999;
                                                                                                                   14-SEP-2000
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(GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 LHKLLGNRWSLIAGRLPGRT 99
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                                                                                                                                                                                                     Cys2His2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 AA;
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                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US32731
                                            99US-0266513.
99US-0149485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0453387
                                                                                                                                                                                                       CCAAT box element; MYB
                                                                                                                                                                                                                                                                                                                                                                              Protein;
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Pred. No.
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Search completed: January 29, 2004, 20:19:33 Job time : 57 secs
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                                                                                                                                                                                                                                                                                                                                             Query Match 6.2%; Score 17; DB 21; Length 48; Best Local Similarity 100.0%; Pred. No. 6.1e-09; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: ball, b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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1 MNSTSMSSLGVRKG
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-461-145C-10
US-09-423-890-13
IS-08-628-829-14
3-09-252-991A-26955
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     summaries
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US-08-467-344A-510
US-08-467-344A-510
US-08-473-49A-510
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US-09-252-991A-22545
US-09-252-991A-21251
US-09-252-991A-21251
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US-09-732-210-373
US-09-732-210-373
US-09-732-210-373
US-09-732-210-373
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US-09-252-991A-32584
US-09-252-991A-2145
US-09-252-991A-2146
US-09-252-991A-2189
US-09-2610-833-2
US-09-2610-833-2
US-09-2610-833-2
US-09-2610-833-2
US-09-2610-833-2
US-09-2610-833-2
US-09-2610-833-2
US-09-2610-833-2
US-09-181-18479
US-09-252-991A-27925
US-09-181-314-2
US-09-252-991A-27925
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US-09-328-352-6616
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US-09-081-975-14
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US-09-156-316-5
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US-09-118-635-19
US-09-018-635-19
US-09-912-962-13
US-09-912-962-13
US-09-912-962-13
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RESULT 2
US-09-610-185C-2
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US-09-610-185C-4
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                                                                                                                                                                   Query Match
Best Local S
Matches 32
Sequence 2, Application US/09610185C Patent No. 6573432
GENERAL INFORMATION:
APPLICANT: Borevitz, Justin
APPLICANT: Xia, Yiji
                                                                                                                                                                                                                                                                                                           SEQ ID NO 4
LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09610185C Patent No. 6573432 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Borevitz, Justin
APPLICANT: Xia, Yiji
APPLICANT: Xia, Yiji
APPLICANT: Dixon, Richard A.
APPLICANT: Lamb, Christopher J.
TITLE OF INVENTION: REGULATION OF ANTHOCYANIN PIGMENT
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: SALKINS.003C1
CURRENT APPLICATION NUMBER: US/09/610,185C
CURRENT FILING DATE: 2000-07-05
CURRENT FILING DATE: 2000-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/603,244
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                 LENGTH: 249
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(249)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                   75
                                                                                                                                          78 LRIHKLIGNRWSLIAGRIPGRTANDVKNYWNT 109
                                                                                                                                                                   32;
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                                                                                                                   LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 106
                                                                                                                                                                     Conservative
                                                                                                                                                                                  100.0%;
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US-09-565-538-1
US-09-561-468-1
US-09-976-165-1
US-09-976-165-1
US-09-976-155-1
US-08-480-258B-1
US-08-480-258B-1
US-08-480-258B-1
US-08-328-352-4586
PCT-US96-08295-1
5466783-2
US-09-107-532A-6397
US-08-480-173A-50
US-08-480-173A-50
US-08-480-173A-50
US-08-484-408A-54
US-09-107-532A-5637
US-09-107-532A-5637
US-09-107-532A-5637
US-09-736-457-791
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Pred. No.
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Sequence
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Seguence
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4586, Appli
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APPLICANT: Dixon, Richard A.
APPLICANT: Lamb, Christopher J.
TITLE OF INVENTION: REGULATION OF ANTHOCYANIN PIC
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: SALKINS.003C1
CURRENT APPLICATION NUMBER: US/09/610,185C
CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: US 09/603,244
PRIOR APPLICATION NUMBER: US 09/603,244
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 248
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Patent No. 5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JOHNSON, TITLE OF INVENTION: TITLE OF INVENTION:
                        APPLICATION NUMBER: PCT/US94/04176
APPLICATION TO APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr. Esq.
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: (FILING DATE: 21-FEB-PRIOR APPLICATION DATA:
                                                                                                               APPLICATION NUMBER: PCT/I
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                           APPLICATION NUMBER: 08/323,460
FILING DATE: 14-Oct-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11690
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 15-May-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 15-Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
REFERENCE/DOCKET NUMBER:
                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 LLGNRWSLIAGRLPGRTANDVKNYWNT 109
||||||||||||||||||||| 106
80 LLGNRWSLIAGRLPGRTANDVKNYWNT 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.9%; Score 27; DB ilarity 100.0%; Pred. No. 2.: Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                      NUMBER: 08/354,516
21-FEB-1995
                                                                                                                                                                                                                                                            UMBER: US 5,405,941
15-Apr-1993
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METHOD AND PRODUCT FOR REGULATING CELL
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                                                                                                   PCT/US94/04178
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CPI-004DVCP2

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Query Match
Best Local Similarity
Thes 8; Conserve
                                                                                                                       TOPOLOGY: linear; MOLECULE TYPE: protein US-08-323-460A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,254
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOVARIK, JOSEPH E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: JOHNSO
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                                                                                                                                                                                                                 TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1247 amino acids
                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1247 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS & MCINTOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 2.9%;
Local Similarity 100.0%;
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TOPOLOGY: linear
                                                                                                                                                                                                                   TELEPHONE: 303/863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1700
CITY: DENVER
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/323,460A FILING DATE: 14-OCT-1994
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ZIP: 80203
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183 LILRLHKL 190
                             76 LILRLHKL 83
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ENTION: METHOD AND PRODUCT FOR REGULATING CELL
ENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                       2.9%; SCC
100.0%; Pr
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                                                            Score 8; DB;
; Pred. No. 22
0; Mismatches
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Pred. No.
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o. 22;
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                                                                                        Length 1247;
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RESULT 5

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Query Match
Best Local Similarity
Watches 8; Conserva
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                                                                                                                                                               RESULT 6
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                                                                                                             Sequence 10, Application US/08461145C Patent No. 6074861
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                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
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PRIOR APPLICATION NUMBER: US 08/354,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield, LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 13
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1247 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY
                                                NUMBER OF SEQUENCES:
                                                               APPLICANT: JOHNSON, GARY L. TITLE OF INVENTION: NOVEL M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
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OPERATING SYSTEM:
SOFTWARE: PatentI
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FILING DATE: 21-FEB-1995
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                76 LILRLHKL 83
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                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catherine
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15-APR-1993
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05-JUN-1995
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                                                                                                                                                                                                                                                                                              2.9%;
                                                               NOVEL MEKK PROTEINS
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Pred. No.
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MEDIUM TYPE: Floppy

COUNTRY: ZIP: 021

02109

Massachusetts

U.S.A.

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US-09-423-890-13
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Matches 8; Conserv
                                                       SEQ ID NO 13
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APPLICATION NUMBER: PCT/US94/11690
ETLING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PCT/US94/04178
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                         PRIOR FILING DATE: 1998-0
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/423,890 CURRENT FILING DATE: 2000-03-06
                                                                                                                                                                                                                             APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: CPI-085CPPC
                                                                                                                                                                                                                                                                                         ENERAL INFORMATION: APPLICANT: CADUS P
                                                                                                                                                                     PRIOR APPLICATION NUMBER:
                                                                                           NUMBER OF SEQ ID NOS
                   TYPE: PRT
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NFORMATION FOR SEQ ID NO:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/461,145C
FILING DATE: 5-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION MADER: US 08/049,254
FILING DATE: 11-APR-1993
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LENGTH: 1247 amino aci
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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                                                                         PatentIn Ver.
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; Pred. No. 22
0; Mismatches
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Query Match
Best Local Similarity
Thes 8; Conserve
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Best Local Similarity
Watches 8; Conserve
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                                                    ; LENGTH: 60
; TYPE: PRT
; ORGANISM: Drosofophila
US-09-058-489-4
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US-09-058-489-4
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                                                                                                                           SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09058489 Patent No. 6103886
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Query Match
Best Local Similarity
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                                                                                                                                        EARLIER APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
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                                                                                                                                                                                                                                                                  APPLICANT: Lahn, Bruce
APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 08/323,460 EARLIER FILING DATE: 1994-10-14
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                                                                                                                                                                                                                                                       FILE REFERENCE: WHI97-08pA
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Whitehead Institute for Biomedical Research
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ITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To External
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2.6%; Score 7; DB 3; 100.0%; Pred. No. 18;
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00.0%; Pred. N
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Pred. No.
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US-08-722-626B-2
; Sequence 2, Application US/08722626B
; Patent No. 5939601
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US-09-252-991A-26955
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SEQ ID NO 26955
LENGTH: 218
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SEQ ID NO 20768
LENGTH: 183
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Patent No. 6551795
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 183
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                            Local
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                                                                                                                                                                            Similarity 7; Conserv
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1998-02-18
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; ORGANISM: Acinetobacter baumannii US-09-328-352-6229
                                                                                                                                                                                                                                                          US-09-328-352-6229
                                                                                                                                                                                                                                                                              RESULT 13
                           Sequence 6229, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6229
LENGTH: 289
TYPE: PRT
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Best Local Similarity
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FILING DATE: 27-SEP-1S
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Klessig, Daniel, F.
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pat Hagan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTSEQ Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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T: 1601 Market Street Suite 720
Philadelphia
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PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 301
TYPE: PRT
ORGANISM: Campylobacter jejuni
US-09-495-406-15
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US-08-671-320-11
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Best Local Similarity 100.0%;
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APPLICANT: Gilbert, Michel

APPLICANT: Wakarchuk, Warren W.

APPLICANT: National Research Council of Canada

APPLICANT: National Research Council of Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09495406 Patent No. 6503744
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                                                                                                                                                                                                   COUNTRY: US
ZIP: 68124-1076
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VIERLII
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VIERLING JR, RICHARD A
TITLE OF INVENTION: A SOVBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1125 SO. 103RD STREET
...
                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                         APPLICATION NUMBER: US/08/671,320 FILING DATE: CLASSIFICATION: 435
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ive 0; Mismatches
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                                                                                  ; MOLECULE TYPE: protein US-08-671-320-11
                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                 INFORMATION FOR SEQ ID NO: 11:
                                                                                              TYPE: amino acids
TOPOLOGY: linear

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233 KLNTTKI 239
                     114 KLNTTKI 120
                     2.6%;
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Conservative
                                         ; Score 7; DB 2
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0; Mismatches
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Search completed: January 29, 2004, 20:21:58
Job time : 32 secs

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Maximum DB
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seq length: 2000000000
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: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep: *
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1 US-09-934-455-390

2 US-10-407-920-29

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2 US-10-021-811-22

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Sequence 482, Appl
Sequence 14, Appl
Sequence 44, Appl
Sequence 438, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 29, Appl
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6 US-10-278-173-14
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7 US-10-008-118A-30
7 US-10-
Sequence 20, Appl
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Sequence 2, Application US/10033190
Publication No. US20020133848A1
GENERAL INFORMATION:
APPLICANT: Exclixis Plant Sciences, Inc.
TITLE OF INVENTION: IDENTIFICATION AND CHARA
TITLE OF INVENTION: TOMATO
FILE REFERENCE: EPO1-002C
CURRENT APPLICATION NUMBER: US/10/033,190
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/244,685
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 274
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; ORGANISM: Lycopersicon esculentum
US-10-033-190-2
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US-10-063-711-88
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Pred. No. 3.8e-265;
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APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
SEQ ID NO 480
LENGTH: 209
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; Publication No. US200
; GENERAL INFORMATION:
; APPLICANT: Adam, Luc
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US-09-934-455-480
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       APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: bubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Keddie, James
APPLICANT: Keddie, James
APPLICANT: Reuber, Lynne
APPLICANT: Reuber, Lynne
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Matches 32
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Jiang, Cai-Zhong
Keddie, James
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Riechmann, Jose Luis
Yu, Guo-Liang
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Ratcliffe, Oliver
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Riechmann, Jose Luis
                                                                                                                                Application US/09934455
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o. US20030121070A1
                                                                                                                                                                                                                                                    11.7%; Score 32; DB ilarity 100.0%; Pred. No. 1.: Conservative 0; Mismatches
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1.2e-23;
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Guo-Liang

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FILE REFERENCE: MBI-0025

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 05/227439

PRIOR APPLICATION NUMBER: 65/227439

PRIOR FILING DATE: 2000-08-22

PRIOR FILING DATE: 2001-08-22

PRIOR FILING DATE: 2001-08-22

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: MBI-0023

PRIOR FILING DATE: 2001-14-17

NUMBER OF SEQ ID NOS: 516

SOFTWARE: PATENTIN Version 3.1

SEQ ID NO 482

LENGTH: 246
                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-934-455-14
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                                                                                                                                                                                                             SEQ ID NO 14
LENGTH: 249
                                                                         Matches
                                                                                               Best Local
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Publication No. US20030121070A1
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Best Local Similarity
                                                                                                             Query Match
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NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
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TLE OF INVENTION: Genes for Modifying Plant Traits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
75 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 106
                     78 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
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                                                                                             Similarity
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Heard, Jacqueline
Jiang, Cai-Zhong
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                                                                           Conservative
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                                                                                           100.0%;
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                                                                                             1.4e-23;
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SOFTWARE: PatentIn Ver.
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/103,312
PRIOR FILING DATE: 1998-10-06
PRIOR PPLICATION NUMBER: 60/108,734
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/113,409
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CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/394,519
PRIOR FILING DATE: 1999-09-13
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT EILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fromm, Mike TITLE OF INVENTION: PLANT GENE SEQUENCES I FILE REFERENCE: MBI-0003
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                                                                     APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
FILE REFERENCE: MBI-0025
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ORGANISM: Arabidopsis thaliana
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mes 32; Conserv
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Jiang, Cai-Zhong
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Dubell, Arnold
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Pilgrim, Marsha
Ratcliffe, Oliver
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Zhang, James
Benito, Maria-Ines
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Reuber, Lynne
Jiang, Cai-Zhong
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Riechmann, Jose Luis
Yu, Guo-Liang
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Adam, Luc
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                                                                                                                                                                                                                                                                                                                     RESULT 8
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LENGTH: 212
TYPE: PRT
SEQ ID NO 6
LENGTH: 120
TYPE: PRT
                                                                                                                                                                                                                                        Sequence 6, Application US/10008118A Publication No. US20020187539A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/443,704
CURRENT FILING DATE: 1999-11-19
CARLIER APPLICATION NUMBER: 60/109,294
EARLIER FILING DATE: NO. US20020066120A1ember 20,
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
                                                                        PRIOR APPLICATION NUMBER: 60/109,294
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 50
                                                                                                                                APPLICANT: Cahoon, Rebecca E.
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 USDIV
CURRENT APPLICATION NUMBER: US/10/008,118A
CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shi, June
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant MYB-Related Transcription Factors
FILE REFERENCE: BB1280 US NA
FILE REFERENCE: BB1280 US NA
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APPLICANT: Rafalski, Antoni
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APPLICANT: Liu, Zhan-Bin
                                                           SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 120
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17; Conserv
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Pred. No. 1.2e-1
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Pred. No.
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hes 0;
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US-10-407-920-29
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                                                                                                                                                                    Sequence 29, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
SEQ ID NO 390
LENGTH: 203
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 203
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                                                           APPLICANT: Shi, Lifang
TITLE OF INVENTION: MYB Transcription Factors
FILE REFERENCE: 38-21(52703)A
CURRENT APPLICATION: NUMBER: US/10/407,920
CURRENT FILLING DATE: 2003-66-06
PRIOR APPLICATION NUMBER: US/60/370,759
PRIOR FILING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT PILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
                                                 NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: MBI-0023 PRIOR FILING DATE: 2001-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEFFERENCE: MBI-0025
                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                    79 RIHKLLGNRWSLIA 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 LLGNRWSLIAGRLPGRT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                               RLHKLLGNRWSLIA 97
                                                                                                                                                                                    Application US/10407920
No. US20040006797A1
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Ratcliffe, Oliver
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Jiang, Cai-Zhong
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7.2e-09;
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                                                                                                                                            and Uses
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Sequence 22, Application US/10021811

Publication No. US20030024007A1

GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Weng, Zude
ITILE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 06/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
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US-10-021-811-22
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PRIOR FILING DATE: 2000-08-22
PRIOR PEPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
SEQ ID NO 70
LENGTH: 219
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ORGANISM: Arabidopsis thaliana
-09-934-455-70
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FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
   OFTWARE: Microsoft Office 97
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Pilgrim, Marsha
Ratcliffe, Oliver
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Jiang, Cai-Zhong
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100.0%; Pred. No. 1.2e-05;
ative 0; Mismatches 0;
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.00.0%; Pred. No.
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        GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REPERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
CURRENT FILING DATE: 2001-12-14
                                                                                                                                                                     Sequence 60, Application US/10021811 Publication No. US20030024007A1
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LENGTH: 115
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
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PRIOR APPLICATION NUMBER: 60/110,609
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NAME/KEY:
LOCATION:
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NAME/KEY:
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NAME/KEY: UNSURE
LOCATION: (113)..(114)
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ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                           61 KSCRLRWLNYLRP 73
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: (112)
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(53)
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100.0%; Pred. No.
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TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13; DB 15;
; Pred. No. 6.8e-05;
                    DB 15;
. 7e-05;
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                                      Length 120;
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Sequence 18, Application US/10021811

Publication No. US20030024007A1

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Fang, Yiwen

APPLICANT: Weng, Ziwen

APPLICANT: Weng, Zude

TITLE OF INVENTION: Plant Myb Transcription Factor Homologs

FILE REFERENCE: BB1294 US NA

CURRENT APPLICATION NUMBER: US/10/021,811

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 60/110,609

PRIOR FILING DATE: 1998-December-02
                                                                                                                                                                                                                                                    ; NUMBER OF SEQ ID NOS: 63; SOFTWARE: Microsoft Office 97; SEQ ID NO 18; LENGTH: 145; TYPE: PRT: ORGANISM: OTYZA BALÍVA US-10-021-811-18
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FEATURE:
LOCATION: (27)
NAME/KEY: UNSURE
LOCATION: (109)
NAME/KEY: UNSURE
LOCATION: (111)
NAME/KEY: UNSURE
LOCATION: (112)
NAME/KEY: UNSURE
LOCATION: (122)
NAME/KEY: UNSURE
LOCATION: (129)
US-10-021-811-60
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NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 60
LENGTH: 131
TYPE: PRT
ORGANISM: Triticum aestivum
Search completed: January 29, 2004, 20:26:32 Job time : 47 secs
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US-10-021-811-18
                                                                                                                                                                  Query Match 4.7%; Score 13; DB 15; Length 145; Best Local Similarity 100.0%; Pred. No. 8.3e-05; Matches 13; Conservative 0; Mismatches 0; Indels
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68 KSCRLRWLNYLRP 80
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
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seq length: 2000000000
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Match
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Gapop 60.0 ,
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hypothetical protein T27F4.12 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change C;Accession: A96689 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; ansen, N.F.; Hughes, B.; Huizar, L.
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. C.A.; Li, J.H.; Li, X.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
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A;Residues: 1-139 <STO>
A;Cross-references: GB;AE005173; NID:g10092496; PIDN:AAG12896.1; GSPDB;GN00141
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Aug-2002
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;Superfamily: Arabidopsis myb-related protein Y19; myb DNA-binding
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                                                                        C.J.; Federspiel, N.A.; Kaul, S:; White, O.; Alonso,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical prote cylm protein - Ent
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flagellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khaykin, E.; Kim, C
Maiti, R.; Marziali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothet
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A;Cross-references: C
C;Genetics:
C;Gene: T27F4.12
A;Map position: 1
                                                                                                                                                       A;Gene: MYB90
C;Superfamily:
C;Keywords: tr
                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-249 KRAA
A;Cross-references: EMBL:AF062915; PIDN:AAC83637.1
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: A96699

A;Status: preliminary

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                             myb-related transcription factor MYB90 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (pate: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: T51687 R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.;
                                                                                                                                                                                                                                                                                                                                                    , Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members
A;Reference number: Z14349; MUID:9839469; PMID:9839469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
T51687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-246 <STO>
                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                 A; Accession: T51687
                                                                                                 Best
                                                                                                                                                         Superfamily: Arabidopsis 28K leaf-specific Keywords: transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                   Query Match
                                                                                                 Local
  75
                                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                          ch 11.7%;
l Similarity 100.0%;
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
LRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:AE005173; NID:g10092494; PIDN:AAG12894.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.7%;
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                                                                            0;
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                                                                                                 Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
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                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; L
2.2e-26;
                                                                                                 DB 2; Le 2.3e-26;
                                                                                                                                                                            myb-related
                                                                                0
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                                                                                                                   Length 249
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                                                                                                                                                                            protein; myb
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                                                                                                                                                                                                                                                                                                                                                                              of the
                                                                                                                                                                                                                                                                                                                                                                                                                                     Denekamp, M.; Greco,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                              Gaps
                                                                                                                                                                                DNA-binding
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Marziali,
                                                                                                                                                                              repeat
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RESULT 4
T51680
myb-related transcription factor MYB75 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51680
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco,
Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members of the R2R3-MYB gene f
A;Reference number: Z14349; MUID:9839469
A;Accession: T51680
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-212 «KRA»
A;Cross-references: EMBL:AF062908; PIDN:AAC83630.1
A;Experimental source: cultivar Columbia
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from

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ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T

ker, M.; Wu, D.; Yu; G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                 R;Loguercio, L.L.; Zhang, J.; Wilkins, T.A. submitted to the EMBL Data Library, November 1997 A;Description: Structure and expression of six classes A;Reference number: Z16842
                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
C;Accession: T09744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transcription factor F25P12.92 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: B96608
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C;Keywords: transcription
                                             A;Gene: Cmy-G
C;Superfamily: unassi
C;Keywords: DNA bindi
F;62-112/Domain: myb
                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues; 1-193 < LOG>
A;Cross-references: EMBL:AF034131; NID:g2921333; PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: Arabidopsis 28K leaf-specific myb-related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: F25P12.92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005173; NID:g9954749; PIDN:AAG09100.1; GSPDB:GN00141
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                                                                                                                                          A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                A;Accession: T09744
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: MYB-like DNA-binding domain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myb-related protein - upland cotton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 27
                                                                                                                                                           Cross-references: EMBL:AF034131; NID:g2921333; PID:g2921334
Experimental source: cultivar Acala SJ-2; ovule
    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 LLGNRWSLIAGRLPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 LIGHRWSLIAGRIPGRTANDVKNYWNT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLGNRWSLIAGRLPGRTANDVKNYWNT 106
                                                                                          unassigned myb DNA-binding repeat proteins;
                                                                       binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                             DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.9%;
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    9.1%;
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                                             repeat homology <MYB>
    Score 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27;
Pred. No.
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Pred. No.
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5e-21;
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5.8e-21;
    DB 2;
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Length 193;
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                                                                                             пyb
                                                                                             DNA-binding
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                                                                                             repeat homol
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A;Accession: T09743
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-198 <LOG>
A;Cross-references: EMBL;AF034130; NID:g2921331; PID:g2921332
A;Experimental source: cultivar Acala SJ-2
C;Genetics:
                                                                                                                                                                                                A;Cross-references: EMBL:AF015269; NID:g2343274; PIDN:AAB67721.1; PID:g2343275
A;Experimental source: cultivar W22
A;Note: the protein is nonfunctional due to insertion of retrotransposon Magel C;Genetics:
A;Gene: Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                            anthocyanin biosynthesis regulatory protein Pl, N;Alternate names: Pl transcription factor C;Species: Zea mays (maize) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myb-related protein - upland cotton
N;Alternate names: MYB-like DNA-binding domain protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
C;Accession: T09743
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T09743
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                                                                                                                                          A;Introns: 34/1; 77/2
C;Superfamily: anthocyanin biosynthesis
F;51-101/Domain: myb DNA-binding repeat
                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-256 < COO>
                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T01189
                                                                                                                                                                                                                                                                                                                                                                  R;Cooper, P.S.; Kent, B.; Matz, E.C.; Cone, K.C. submitted to the EMBL Data Library, July 1997 A;Description: Pl-987: a nonfunctional maize anthocyanin A;Reference number: Z14257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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C;Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat homolog
C;Keywords: DNA binding
F;63-113/Domain: myb DNA-binding repeat homology <MYB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1997 A;Description: Structure and expression of six classes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Loguercio, L.L.;
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                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T01189
                                                                       Matches
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                                79 RLHKLLGNRWSLIAGRLPGRT 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              #sequence_revision 12-Feb-1999
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Pred. No.
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89
                                                                       Mismatches
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                                                                                                                                              homology
                                                                                                                                                               regulatory protein; myb
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RYCONE, K.C.; Cocciolone, S.M.; Moehlenkamp, C.A.; Weber, T.; Drummond, B.J.; Tagliani, Plant Cell 5, 1807-1816, 1993

Plant Cell 5, 1807-1816, 1993

A;Title: Role of the regulatory gene pl in the photocontrol of maize anthocyanin pigment A;Reference number: Z15034; MUID:94138244; PMID:8305873

A;Accession: T03974

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-264 <CON>
A;Cross-references: EMBL:L19496; NID:g309571; PIDN:AAA19819.1; PID:g309572

A;Experimental source: strain Tx303

C;Genetics: 45/1; 88/2

C;Function:
              C;Specie
C;Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C;Accession: T03974
                                                                                            RESULT
T01188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C;Accession: T03972
R;Cone, K.C.; Cocciolone, S.M.; Moehlenkamp, C.A.; Weber, T.; Drummond, B.J
Plant Cell 5, 1807-1816, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: transcriptional activator for anthocyanin biosynthesis C;Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-b: F;9-61/Domain: myb DNA-binding repeat homology <MYB>
                                                                                                                                                                                                                                                                                                                                     A;Description: transcriptional activator for anthocyanin biosynthesis C;Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-b:F;9-61/Domain: myb DNA-binding repeat homology <MYB>F;62-112/Domain: myb DNA-binding repeat homology <MYB1>
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A;Experimental source: strain McClintock
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A; Residues: 1-266 < CON>
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                                                    N;Alternate names: Pl
                                                                       anthocyanin biosynthesis regulatory
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Best Local S
Matches 21
              ;Species: Zea mays
;Date: 12-Feb-1999
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Best Local
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#sequence_revision 12-Feb-1999 #text_
                                                    transcription
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Pred. No.
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Pred. No.
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factor
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A; Cone, P.S.; Kent, B.; Matz, E.C.; Cone, K.C. submitted to the EMBL Data Library, July 1997
A; Description: P1-987: a nonfunctional maize anthocyanin regulatory gene resulting from 1 A; Reference number: Z14257
A; Accession: T01188
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-267 < CCO>
A; Cross references: EMBL: AF015268; NID: 92343272; PIDN: AAB67720.1; PID: 02747777
A; Experimental source: Cultivar W22
C; Genetics:
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T03715
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R;Kranz, H.D.; Denekamp, M.; ; Paz-Ares, J.; Weisshaar, B. Plant J. 16, 263-276, 1998
                                                                                         C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: transcriptional activator for anthocyanin biosynthesis C;Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-binding F;9-61/Domain: myb DNA-binding repeat homology <MYB> F;62-112/Domain: myb DNA-binding repeat homology <MYB1>
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C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Cocciolone, S.M.; Cone, K.C. submitted to the EMBL Data Library, April 1993 A;Description: Pl-Bh, an anthocyanin regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anthocyanin biosynthesis regulatory protein Pl-Bh - C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
C;Accession: T03715
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                                                                                                                                                    probable transcription factor MYB82 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
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A; Note: Pl-Bh (Blotched1)
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A; Residues: 1-271 <C
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A; Introns: 45/1;
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Pred. No.
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Pred. No.
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                                                              R.;
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2e-14;
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                                                           Kranz, H.D.;
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myb-related 24.7K transcription factor - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_changes.
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S71287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Ransen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
Nature 408, 816-820, 2000
Rature 408, 816-820, 2000
Nature 408, 816-820, 816, 816
Nature 408, 816-820, 816, 816
Nature 408, 816, 816
Nature 408, 816-820, 816, 816
Nature 408, 816-820, 816
Nature 408, 8
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C;Accession: F96734
R;Theologis, A.; Ecker, J.R.; Palm,
R;Theologis, A.; Conn, L.;
R;Kirik, V.; Baeumlein, H.:
Gene 183, 109-113, 1996
A;Title: A novel leaf-specific myb-related protein with a A;Reference number: JC5729; MUID:97149286; PMID:8996094
                                                                                                                                                                                                                                                                                                                          R;Kirik, V.; Baumlein, H.
submitted to the EMBL Data Library, December 1995
A;Description: Isolation and chromosomal localization of leaf-specific cDNA encoding
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A;Residues: 1-130 <KKA>
A;Cross-references: EMBL:AF062912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from ArA;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
C;Superfamily: Arabidopsis myb-related 24.7K protein; myb DNA-binding
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: MYB82
                                                                                                                                                A;Residues: 1-213 <KIR>
A;Cross-references: EMBL:Z68157; NID:g1197189; PIDN:CAA92280.1;
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A;Accession: S71287
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Residues: 1-195 <STO>
;Cross-references: GB:AE005173; NID:g6714312; PIDN:AAF26005.1; GSPDB:GN00141
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Best Local 9
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100.0%; Prr
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k; Pred. No. 3.2
0; Mismatches
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Pred. No.
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3.2e-10;
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Marziali,
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A;Accession: JC5729
A;Molecule type: mRNA
A;Residues: 1-213 <KI2>
A;Cross-references: EMBL:Z68157; NID:g1197189; PIDN:CAA92280.1; PID:g1197190
C;Comment: This protein is involved in the control of anthocyanin biosysthesis and the C;Genetics:
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                                                                                                                                                            C;Superfamily: Arabidopsis myb-related 24.7K protein; myb DNA-binding repeat homology C;Keywords: DNA binding; nucleus; transcription regulation F;30-80/Domain: myb DNA-binding repeat homology <MYBZ> F;54-80/Region: helix-turn-helix
                                                                                                                                                                                                                                                                     A;Gene: AtmybL2
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Best Local Similarity
                         83 LLGNRWSLIAGRLPGRT 99
52 LLGNRWSLIAGRLPGRT
                                                                          6.2%; Solitarity 100.0%; If Conservative 0;
68
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Pred. No.
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Nuclear protein; DNA-binding; Repeat;
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"Molecular analysis of the C1-I allele
mutant of the regulatory C1 locus.";
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                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CONTROLS THE EXPRESSION OF GENES INVOLVED IN ANTHOCYANIN BIOSYNTHESIS. REGULATES THE EXPRESSION OF AT LEAST 3 STRUCTURAL GENES: CHALCONE SYNTHASE, DIFYDROELAVONOL REDUCTASE AND FLAVONOL O(3) GLUCCOSYLTRANSFERASE. C1 ACTS AS A TRANS-ACTING FACTOR. SUBCELLULAR LOCATION: Nuclear (Probable). MISCELLANEOUS: THE C1-1 ALLELE IS A DOMINANT NEGATIVE MUTANT WHICH INHIBITS PIGMENT FORMATION.
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AC Q9FTA2;

AC Q9FTA2;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT TRANSPARENT TESTA 2 protein (Myb-related protein 123) (AtMYB123) (Myb-

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DNA_BIND
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence features of the rephysically assigned P1 and DNA Res. 5:297-308(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stracke R., Werber M., Weisshaar B.; "The R2R3-MYB gene family in Arabidopsis thaliana."; Curr. Opin. Plant Biol. 4:447-456(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND MUTANTS TT2-2 AND STRAIN=cv. Columbia, cv. Landsberg erecta, MEDLLNE=21434422; Pubmed=11549766; MEDLLNE=21434422; Pubmed=11549766; MEDLLNE=21434420; Pubmed=11549766; Median Todd Columbia Median M
This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
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Nakamura Y., Sato S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
MEDLINE=21481677; PubMed=11597504;
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                                                                                                                                                                                                                                                                                                                   FUNCTION: Transcription factor involved in the cor flavonoid late metabolism in developing siliques. in determining the tissue-specific activation of leucoanthocyanidin reductase (BANYULS). SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Expressed at a high level in i and at a lower level in flowers. Undetected in you
                                                                                    SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                             completion of MISCELLANEOUS:
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DEVELOPMENTAL STAGE: Highly expressed from of embryogenesis to the globular stage, dec the late heart-torpedo stage and did not pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N., Jond C., Debeaujon I., Caboche M., Lepiniec L.;
Arabidopsis TT2 gene encodes an R2R3 MYB domain protein that ackey determinant for proanthocyanidin accumulation in developing
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MYB 2.
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European Bioinformatics Institute.

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RESULT 3
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Matches 17
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DNA_BIND 11 63 MY
DNA_BIND 64 114 MY
NP_BIND 47 54 AT
VARIANT 174 1.74 Q
MUTAGEN 66 66 G-
                                                                                                                                                                                                                                                                                                                                                                                                                  MYBC MAIZE
P10290;
01-MAR-1989
01-MAR-1989
28-FEB-2003
        This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.
                                                                                                        Paz-Ares J., Ghosal D., Wienand U., Peterson P.A., Saedler H.;
"The regulatory of locus of Zea mays encodes a protein with homology
to myb proto-oncogene products and with structural similarities to
transcriptional activators.";
EMBO J. 6:3553-3558 (1987).
-!- FUNCTION: CONTROLS THE EXPRESSION OF GENES INVOLVED IN ANTHOCYANJ
BIOSYNTHESIS. REGULATES THE EXPRESSION OF AT LEAST 3 STRUCTURAL
GENES: CHALCONE SYNTHASE, DIHYDROPLAVONOL REDUCTASE AND FLAVONOL
0(3) GLUCOSYLTRANSFERASE. C1 ACTS AS A TRANS-ACTING FACTOR.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Panicoldeae; Andropogoneae; Zea.
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PROSITE; PS00037; MYB 1; 1.

PROSITE; PS00334; MYB 2; 1.

PROSITE; PS50090; MYB 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ299452; CAC40021.1; -.
EMBL; AB737191; AAK54744.1; -.
EMBL; AB015477; AB0808716.1; -.
HSSP; P06876; 1MBK.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=88111545; PubMed=3428265;
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(Rel. 10, Last sequence update)
(Rel. 41, Last annotation updat
regulatory C1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rmatics Institute. There are institutions as long as its atement is not removed. Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYB 2.
ATP (POTENTIAL).
Q -> L (IN CV. WS).
G->R: IN TT2-4; LOSS O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIGMENTATION.
MISSING: IN TT2-2; REDUCED PIGMENTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3BA9CB3F723D1C2E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273
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                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; L
6.9e-10;
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                                                  and the EMBL outst
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                                                                    a collaboration
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           for commercial 
ib.ch/announce/
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RESULT 4
GL1_ARATH
      REAL RESERVE TO THE REAL PROPERTY OF THE REAL PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GL1 ARATH STANDARD; PRT; 228 AA P27900; Q9ST42; 01-AUG-1992 (Rel. 23, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat Trichome differentiation protein GL1 (GLABR
                                                                                                                                MEDLINE=21396402; PubMed=11504855; Hauser M.T., Harr B., Schlotterer C.; "Trichome distribution in Arabidopsis Arabidopsis lyrata: molecular analysis GLABROUS1.";
STRAIN=cv. Columbia;
MEDLINE=20363099; PubMed=10907853;
Kaneko T., Katoh T., Sato S., Naka
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia;
MEDLINE=99449058; PubMed=10520748;
Shikazono N., Tanaka A., Yokota Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92034971; PubMed=1934056;
MEDLINE=92034971; PubMed=1934056;
Oppenheimer D.G., Herman P.L., Sivakumaran
"A myb gene required for leaf trichome diff
is expressed in stipules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMĀIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00034; MYB 3; 2.
PROSITE; PS50090; MYB 3; 2.
Nuclear protein; DNA-Binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001005; Myb_DNA_bi; Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia,
                                                                                                                                                                                                                                                                                                                                                         ecotype Columbia.
                                                                                                                                                                                                                                                                                                                                                                         Shikazono N., Tanaka A., Yokota Y., Wa
"Nucleotide sequence of the GLABROUS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GL1 OR AT3G27920 OR K16N12.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; T01592; -. MaizeDB; 24964; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S06215; TVZMMB.
HSSP; P01103; 1POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M37153; AAA33482.1; -.
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67:483-493 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 LLGNRWSLIAGRLPGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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                                                                                                                                                                                                                                                                                                                                       9:177-181 (1998).
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9 61 MYB
62 112 MYB
205 212 POL
234 273 ASP
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234
273 AA;
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                                                                                                             18:1754-1763 (2001)
                                                                                                                                                                                                                                                                  CV.
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  Sato S., Nakamura
                                                                                                                                                                                                                                                                Ba-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                           Yokota Y., Watanabe H., Tano S.; he GLABROUS1 gene of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
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MYB 2.
POLY-GLY:
ASP/GLU-RICH (ACIDIC
ASP/GLU-RICH (ACIDIC
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Pred. No.
                                                                                                                                                       analysis
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                                                                                                                                                                                                                                                                Bla-1,
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(GLABROUS1
                                                                                                                                                                                thaliana
  Α.,
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differentiation
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7.2e-10;
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    Asamizu
                                                                                                                                                         candidate
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    Tabata
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                                                                                                                                                                                                                                                                                                                                                                                  thaliana
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RESULTY
MYB1_HO
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AC P2
DT 011
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DE MY
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Best Local
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EMBL; AB006078; BAA86879.1; -.
EMBL; AF263690; AAL01215.1; -.
EMBL; AF263690; AAL01218.1; -.
EMBL; AF263691; AAL01219.1; -.
EMBL; AF263695; AAL01220.1; -.
EMBL; AF263695; AAL01220.1; -.
EMBL; AF263697; AAL01227.1; -.
EMBL; AF263697; BAB02538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00249; myb_DNA-binding;
SWART; SW00717; SRANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
Nuclear protein; DNA-binding; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             MYB1_HORVU
P20026;
                                                          STRAIN-CV. Abyssinian 2231;
STRAIN-CV. Abyssinian 2231;
MEDLINE=89313655; PubMed=2664447;
MEDLINE=89313655; PubMed=2664447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
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                                                                                                                                                                                                Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                     MYB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use
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                                                                                                                                                                                                                                                                                                                                                                                                                                         HORVU
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Pfam; PF00249; myb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T01588; -. InterPro; IPR001005;
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Sequence features of
                                            Marocco A., Wissenbach M., Salamini F., Rohde W.;
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          Myb-related
                                                                                                                                                                                                                                                                                                                              01-FEB-1991
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
                      "Multiple
                                                                                                                                                                          NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Res. 7:217-221(2000)
FUNCTION: REGULATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAC clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIFFERENTIATE
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P01103; 1POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLHKLLGNRWSLIA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLHKLLGNRWSLIA 92
genes are transcribed in Hordeum vulgare and DNA binding domain of the myb oncoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AA;
                                                                                                                                                                                                                                                                                                                            (Rel. 17,
(Rel. 17,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
64
149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: Nuclear
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114
149
224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.1%;
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Last
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-binding; 2.
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                                                                                                                                                                                                                       Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                  annotation
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Pred. No.
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MYB 2.

C -> R (IN REF. 1).

GDV -> SDI (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822A8646F446F6B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation.
                                                                 Paz-Ares J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.2e-07
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PRIMORDIA TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                     Saedler
                          Zea
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                          mays
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RESULT MYBP MA ID MY BP 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P27898; P27899;
01-AUG-1992 (Rel
01-AUG-1992 (Rel
01-FEB-2003 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
PACCAD clade; Panicoideae; Andropogoneae;
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X70877; CAA50222.1; -.
EMBL; X70877; CAA50224.1; -.
EMBL; S61506; S61506.
HSSP; P01103; 1POM.
                               MEDLINE=91271238; PubMed=2052542;
Grotewold E., Athma P., Peterson T.;
"Alternatively spliced products of the maize P gene encode proteins
with homology to the DNA-binding domain of myb-like transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T02887; -.
InterPro; IPR001005; Myb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant J. 4:411-422(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chimeric Myb
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                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Myb-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00249; myb_DNA
SMART; SM00717; SANT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myb genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94035190; PubMed=8220488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYBP_MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear (Probable) TISSUE SPECIFICITY: GERMINATING SEED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: POSSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTERNAL SIGNAL. MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Similarity 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSLIAGRIPGRT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
267 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from Hordeum vulgare: tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abyssinian
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 23, Created)
(Rel. 3, Last sequence update)
(Rel. 41, Last annotation update)
protein P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter/Gus genes in transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ueberlacker B., Vogt F., Becker D., Salamini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
112
29740 Þ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2231; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTION AY BE INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s; Score 12; DB
s; Pred. No. 0.0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYB 1.
MYB 2.
DBECEDCEBA847749 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVATOR IN RESPONSE IN THE REGULATION OF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; L
0.00011;
                                                                                                                                                                                                                                                                          Embryophyta; Tracheophyta;
a; Poales; Poaceae;
e; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MERISTEM OF SHOOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E TO AN
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RESULT
M3K4_M
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Best Local S
Matches 9
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Pfam; PF00249; myb_DNA-binding; 2.

SMART; SM00717; SANT; 2.

PROSITE; PS00037; MYB 1; 1.

PROSITE; PS00334; MYB 2; 1.

PROSITE; PS00334; MYB 3; 2.

NICTORY PROSITE; PS0090; MYB 3; 2.
.M3K4 MOUSE STANDARD; 
OO8648; OO8649; O70124;
30-MAY-2000 (Rel. 39, Created)
                           MOUSE
                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                                                                                                                    EMBL; M73028; AAA33500.1; -.
EMBL; M73029; AAA33501.1; -.
EMBL; M73029; CAA77939.1; -.
EMBL; Z11879; CAA77939.1; -.
PIR; A39697; A39687.
PIR; B39697; B39697.
                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics 131:199-209(1992).
-!- FUNCTION: TRANSCRIPTION FACTOR POSTULATED TO BIOSYNTHETIC PATHWAY OF A FLAVONOID-DERIVED
                                                                                                                                 SEQUENCE
                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           MaizeDB; 69180; -.
MaizeDB; 69181; -.
                                                                                                                                                                                                                                                                                                                             TRANSFAC; T01590; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transposition of Ac.";
                                                                                                                                                                                                                                      Alternative splicing
                                                                                                                                                                                                                                                Nuclear
                                                                                                                                                                                                                                                                                                                                               HSSP; P01103; 1POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Insertional mutagenesis of the maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Athma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear (Probable) ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLORAL TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P27898-2; Sequence=VSP_003301, VSP_003302;
.MILARITY: Contains 2 Myb-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P27898-1; Sequence=Displayed;
                                                                              84
                                                                                              Similarity
9; Conserv
                                                                                                                                                                                                                                              protein; DNA-binding; Repeat;
                                                                       LGNRWSLIA 92
                                                             LGNRWSLIA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grotewold
                                                                                                                                  399
                                                                                                                                                  153
                                                                                                                                                                                            178
305
                                                                                               Conservative
                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=1317315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sci.
                                                                                                                                                                                            61
112
181
311
152
                                                                                                                                                  399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E., Peterson
                                                                                                                                  43756
                                                                                                      100.0%;
                                                                                                                3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                 WW.
                                                                                              Score 9; DB 1; Pred. No. 0.2 0; Mismatches
                                                                                              ٥,
                                                                                                                                                                          POLY-LEU.
WSLIASHEGRTDNEIKNYWNSHLSRQIHTYRRKYTAGEDD
TAIAIDMSKLOSADRRRGGRTPG -> RHLMIEADYSBPST
VRCLERGALAYLTLPRQSPFQTARITYDRIGSALLRSVRFC
                                                                                                                                         Missing (i
/FTId=VSP_
                                                                                                                                                         FRCVPSRW (in isoform Short).
/FTId=VSP_003301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88:4587-4591(1991).
                  PRT;
                                                                                                                                 EE025B00A44CF5D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
                                                                                                                                               (in isoform Short).
                                                                                                      DB 1;
o. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ש
                                                                                                                                                                                                                                                Transcription regulation;
                                                                                                                                        _003302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene by intragenic
                   AA
                                                                                              0:
                                                                                                                Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO REGULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIGMENT
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IN CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gh a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE
                                                                                              0
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 no
                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                              0;
 NP_BIND
BINDING
ACT_SITE
                          DOMAIN
                                            Transterase;
Alternative :
                                     DOMAIN
```

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

Serine/threonine-protein kinase;

ATP-binding;

POLY-ALA.

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EMBL; U85607;
EMBL; U85608;
EMBL; U66240;
HSSP; P24941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6; TISSUE=Ectoplacental cone; MEDLINE=97422605; PubMed=9268631; Schweifer N., Valk P.J., Delwel R., Cox R., Meier-Ewert S., Lehrach H., Barlow D.P.; "Characterization of the C3 YAC contig from 17 and analysis of allelic expression of gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Mitogen-activated protein kinase kinase kinase 4 (EC
(MAPK/ERK kinase kinase 4) (MEK kinase 4) (MEKK 4).
MAP3K4 OR MEKK4.
Pfam; PF00069; pkinase; 1.

ProDom; PD00001; Prot_kinase; 1.

SMART; SM00220; S TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENOMICS 43:285-297(1997).
-I- FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAPK PATHWAYS, BUT NOT THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES MAP2K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerwins P., Blank J.L., Johnson G.L., "Cloning of a novel mitogen-activated MEKK4, that selectively regulates the
                                                                                                                                                                                                     EMBL; U66240; AAC08286.1;
HSSP; P24941; 1HCL.
MGD; MGI:1346875; Map3k4.
                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 363-1049 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathway."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97236778; PubMed=9079650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY:
SKELETAL MUSCLE, KII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: LOCALIZED IN PERINUCLEAR STRUCTURES, PROBABLY GOLGI-ASSOCIATED VESICLES ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKELETAL MUSCLE, KIDNEY, TESTIS FOLLOWED LOW EXPRESSION WAS FOUND IN SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND MAP2K6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=008648-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=008648-2; Sequence=VSP_004885;
SSUE SPECIFICITY: WIDELY EXPRESSED. HIGH EXPRESSION WAS FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem.
                                                                                                                                                                                                                                                       ; AAC53126.1; -.; AAC53127.1; -.
. AAC53127.1; -.
                                                                                                                                                                                                                               AAC08286.1;
1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272:8288-8295(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein kinase kinase kinase,
c-Jun amino terminal kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rom proximal mon
genes flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Francis F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.7.1.-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M3K4 HUMAN STANDARD; PRT; 1607 AA.

Q9Y6R4; Q92612;

30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

38-FEB-2000 (Rel. 41, Last annotation update)

Mitogen-activated protein kinase kinase kinase 4

(MAPK/ERK kinase kinase 4) (MEK kinase 4) (MEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 8
HUMAN
This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., ALTERNATIVE SPLICING, TISSUE-Fetal liver, and Skeletal muscle; MEDLINE=97449143; PubMed=9305639; Takekawa M., Posas F., Saito H.; Takekawa M., Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Prediction of the coding sequences of unidentified human The coding sequences of unidentified human The coding sequences of KIRAO201-KIRAO280) analysis of CDNA clones from cell line KG-1 and brain."; DNA Res. 3:321-329(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAP3K4 OR MAPKKK4 OR MEKK4
                                                                                                                                                                                                                                                               +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97191544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 68-1607 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 16:4973-4982(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTK1, mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                  IsoId=Q9Y6R4-2; Sequence=VSP 004884; TISSUE SPECIFICITY: EXPRESSED \overline{A}T HIGH LEVELS IN HEART, PLACENTA, SKELETAL MUSCLE AND PANCREAS, AND \overline{A}T LOWER LEVELS IN OTHER TISSUES.
                                                                                                                                                                                        SIMILARITY: BELONGS TO THE SER/THR FAMILY KINASE KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                 DOMAIN: THE N-TERMINAL NON-CATALYTIC DOMAIN (1-606) CONTAINS & ESSENTIAL DOMAIN FOR THE DOMINANT-INHIBITORY EFFECT. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ACTIVATES THE CSBP2, P38 AND JNK MAPK PATHWAYS, I THE ERK PATHWAY. SPECIFICALLY PHOSPHORYLATES AND ACTIVATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND MAP2K6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 LILRLHKL 540
                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9Y6R4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LILRLHKL
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473
1597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seki N., Ishikawa K.-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Human) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stress-induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9039502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364
473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 8; DB 1
%; Pred. No. 8.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
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/FTId=VSP_004885.
SL -> NS (IN REF. 2).
T -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ssk2/Ssk22 MAP kinase kinases activation of the p38 and JNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E84AEAAE92D103A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawarabayasi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAP three kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.7.1.-)
                                                                        restrictions
tent is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF LYS-1371
                                                                                                                         a collaboration
                                                     for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAP2K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 9
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Best Local :
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                                   SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMede7542800;

MEDLINE=95350630; PubMede7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., Fi. Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Frine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine L.D., Fritchman J.L., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
ACT SITE
                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrate/nitrite response regulator protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S TKc; 1.
PROSITE; PS00100; PROTEIN_KINASE_ATP; 1
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF002715; AAB68804.1; -.
EMBL; D86968; BAA13304.1; -.
PIR; T03022; T03022.
HSSP; P24941; 1HCL.
                                                                                                                                                                                                                   Haemophilus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                          NARP OR HI0726
                                                                                                                                                                                                                                                                                                        P44845;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0006950; P:respons
InterPro; IPR000719; Prot
InterPro; IPR002290; Ser
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          Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                 NARP_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM;
                                                                                                                                                                                                       NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                 "Whole-genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0004709; P:MAP kinase kinase kinase activity; GO:0000186; P:activation of MAPKK; TAS. GO:0007254; P:JNK cascade; TAS.
FUNCTION: COULD ACTIVATE THE
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1371
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791
1607
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                                  random sequencing
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181550 ⊳
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                                                                                                                                                                                                                                                                                                                                                                                                                     83
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1201
1600
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1371
1462
1223
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POLY-ALA.
PROTEIN KINASE.
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Pred. No.
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K->R: LOSS OF ACTIVITY.
I -> R (IN REF. 2).
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ATP (BY SIMILARITY).
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EXPRESSION OF
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                                   of Haemophilus influenzae
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AND COULD REPRESS THE TRANSCRIPTION OF THE

FUMARATE

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NARP ECOLI
ID NARP ECOLI
AC P31802;
DT 01-JUL-1993
DT 01-JUL-1993
DT 28-FEB-2003
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   REAR RELEASE OF THE RELEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000792; HTH_LuxR.
InterPro; IPR001789; Response_reg.
Pfam; PF00196; GerE; 1.
Pfam; PF00072; response_reg; 1.
Pfam; PF000038; HTHLUXR.
PRINTS; PR00038; HTHLUXR; 1.
ProDom; PD000307; HTH_LUXR; 1.
ProDom; PD0003039; Response_reg; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00421; HTH_LUXR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U1-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrate/nitrite response regulator protein narp.
NARP OR B2193.
                                                                                                                                                                                                             "Dual response regulators (NarL and NarP) interact with dual sensors (NarX and NarQ) to control nitrate- and nitrite-regulated gene expression in Escherichia coli K-12.";
J. Bacteriol. 175:3259-3268(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00622; HTH LUXR FAMILY; 1.

PROSITE; PS50110; RESFONSE REGULATORY; 1.

Transcription regulation; Activator; Repressor; DNA-binding; ACTIVATOR; PROSIDER FACTOR; Complete property of the property o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a licence
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93273691; PubMed=8501030; Rabin R.S., Stewart V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32756; AAC22384.1; PIR; A64089; A64089.
Submitted (OCT-1993) to
                                 Richterich P., Lakey Church G.M.,
                                                                                                        STRAIN=K12
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P10957; 1RNL.
TIGR; HI0726; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
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REDUCTASE (FRDABCD) C
- SIMILARITY: Contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATORS.
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                                                                                                            BHB2600;
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the EMBL/GenBank/DDBJ databases
                                                                   Gryan G., Jaehn L., Mintz L., Robison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gammaproteobacteria; Enterobacteriales;
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Pred. No.
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PSB2 CEPAL

AC Q0082
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OS CEPAL
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Best Local S
Matches 7
                                                                  PSB2 CRYNE
Q00826;
16-OCT-2001
16-OCT-2001
28-FEB-2003
Probable pro
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SMART; SMO0448; REC; 1.

PROSITE; PS00622; HTH LUXR FAMILY; 1.

PROSITE; PS00622; HTH LUXR FAMILY; 1.

PROSITE; PS00622; HTH LUXR FAMILY; 1.

Transcription; RESPONSE REGULATORY; DNA-binding; Proposition; Sensory transduction; ATP-binding; Phosphorylation; Sensory transduction; Nitrate assimilation; Complete proteome.

Nitrate assimilation; Complete proteome.

RESPONSE REGULATORY.

PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a clear the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
   Cryptococcus neoformans
Eukaryota; Fungi; Basidi
Tremellomycetidae; Treme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00038; HTHLUXR.

ProDom; PD000397; HTH LuxR; 1.

ProDom; PD000039; Response_reg;

SMART; SM00421; HTH LUXR; 1.

SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose [Mau B., Shao Y.]
                                                                                                                                                                            CRYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00196; GerE; 1.
Pfam; PF00072; response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EcoGene; EG11527; narP.
InterPro; IPR000792; HTH LuxR.
InterPro; IPR001789; Response_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U00008; AAA16411.1; ALT_INIT.
EMBL; AE000309; AAC75253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L11273; AAA24200.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P10957; 1RNL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A40584; A40584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THIS PROTEIN ACTIVATES THE EXPRESSION OF THE NITRATE REDUCTASE (NARGHJI) AND FORMATE DEHYDROGENASE-N (FDNGHI) OPERONS AND REPRESSES THE TRANSCRIPTION OF THE FUNARATE REDUCTASE (FRDABCD) OPERON IN RESPONSE TO A NITRATE/NITRITE INDUCTION SIGNAL TRANSMITTED BY EITHER THE NARX OR NARQ PROTEINS.

SIMILARITY: Contains 1 response regulatory domain.

SIMILARITY: BELONGS TO THE LUXE/UHPA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 response regulatory domain.
SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL REGULATORS. SIMILAR TO THE NARL PROTEIN.
                                                                                                                                                                                                                                                 191 NLLRKLN
                                                                                                                                                                                                                                                                             110 NLLRKIN 116
                                                                                                                                                                                                                                                                                                               l Similarity
7; Conserv
                                                                      proteasome
                                                                                                                                                                                                                                                                                                                                                                                    171
215 AA;
                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
steasome subunit beta type 2 (EC 3
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                          STANDARD;
Basidiomycota; Hymenomycetes; Heterobasidio; Tremellales; Tremellaceae; Filobasidiella
                                                                                                                                                                                                                                                                                                                                                                                    190 I
23575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Response_reg.
                                                                                                                                                                                                                                                                                                                                                   2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _reg; 1.
                   (Filobasidiella neoformans).
omycota; Hymenomycetes; Heterobasidiomycetes;
                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                               Score 7; DB 1; Pred. No. 15; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARI'
H-T-H MOTIF (BY SIMILARITY).
; C7121668E3130956 CRC64;
                                                                                                                                                            224
                                                                                                                                                                                                                                                                                                                       DB
. 15;
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                                                                                                                                                          B
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                                                                       3.4.25.1).
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yhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.J.,
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RESULT 12
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Best Local (
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000243; Proteasome_B.
InterPro; IPR001353; Protease_protease.
Pfam; PF00227; proteasome; 1.
PROSITE; PS00854; PROTEASOME_B; FALSE_NEG.
Proteasome; Hydrolase; Protease.
SEQUENCE 224 AA; 25239 MW; ABEEF03E761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                     MEDLINE=89313655; PubMed=2664447;
Marocco A., Wissenbach M., Becker D.,
Salamini F., Rohde W.;
                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Las 28-FEB-2003 (Rel. 41, Las Myb-related protein Zm38. Zea mays (Maize).
                                                                                                                                                                                                                                                                             MYB3_MAIZE
P20025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L40028; AAB06582.1;
HSSP; P22141; 1RYP.
MEROPS; T01.984; -.
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                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chang Y.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96239006; PubMed=8675296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ect. Immun. 64:1977-1983(1996).

ect. Immun. 64:1977-1983(1996).

WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR SLICHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC ACTIVITY (BY SIMILARITY).

CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteolytic pathway.
SUBUNIT: THE PROTEASOME IS
SUBUNITS WHICH FORM A HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic and nuclear SIMILARITY: Belongs to peptidase family TIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specificity.
PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal
                                                                                                                                                                                                                                                                                                                                                                  160 LLRKCID 166
                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 LLRKCID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for virulence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penoyer L.A., Kwon-Chung K.J.; capsule gene of Cryptococcus neoformans, CAP64,
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             29
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                                                                                                                                                                                                                                                                                                                                                                                                                                      2.6%;
                                                                                                                                                                                                                                  Last
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                                                                                                                                                                                                                                  annotation
                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOSED OF AT LEAST 15 NON IDENTICAL LY ORDERED RING-SHAPED STRUCTURE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A8EEF03E76170886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                         255
                                                                                  Paz-Ares J.,
                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                    Saedler
                                                         Zea mays that
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MYB3 HORWI

MYB3 HORWI

MYB3 HORWI

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GN MYB2.

GN MYB2.

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Best Local
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P20027;
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994
16-OCT-2001
Myb-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWART; SMOULY; MYB 1; 1.

PROSITE; PS00037; MYB 2; 1.

PROSITE; PS00334; MYB 3; 2.

PROSITE; PS50090; MYB 3; 2.

Nuclear protein; DNA-binding; Repeat; Transcription regulation.

MYB 1.
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                                                                                                                                                                                                                                                                                                                                                     "Multiple genes are transcribed in Hordeum vulgare and Zea mays that carry the DNA binding domain of the myb oncoproteins.";
Mol. Gen. Genet. 216:183-187(1989).
-1- FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR IN RESPONSE TO AN EXTERNAL SIGNAL. MAY BE INVOLVED IN THE REGULATION OF FLAVONOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T02959; -.

MaizeDB; 69594; -.

InterPro; IPR001005; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 2.

SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Abyssinian 2231;
MEDLINE=89313655; PubMed=2664447;
MAROCCO A., Wissenbach M., Becker D., Paz-Ares J.,
Salamini F., Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. Abyssinian 2231; TISSUE-Leaf; MEDLINE-94035190; PubMed-8220488; Wissenbach M., Ueberlacker B., Vogt F., Dolan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HORVU
                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 35-302 FROM N.A. STRAIN=cv. Abyssinian 2231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Myb genes from Hordeum vulgare: tissue-specific chimeric Myb promoter/Gus genes in transgenic tob Plant J. 4:411-422(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare (Barley).
Eukaryota, Viridiplantae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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HSSP; P01103; 1POM.

    -!- SIMILARITY: Contains 2 Myb-like domains.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear () TISSUE SPECIFICITY: GERMINATING
                                                                                                                                                                                                                                                                                                                                      BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
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7; Conserv
                                                                                                                                                                                                                                                                 ROOT
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
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yta; Liliopsida; Poales; Poaceae; Pooidea
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WG SEED AND
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18;
                                                                                                                                                                                                                                                                                                                                                                                                                               eum vulgare and oncoproteins.";
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                                                                                                                                                                   collaboration -
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EMBL; X70881; CAA50226.1; -.

CAA50223.1;

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RESCILIT YARCULUT YARC ILIT YARCH IL
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Rabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Rabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Rabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Rabret C., Ferrari E., Foulger D.,
RA Choi S.K., Glaser P., Goffeau A., Golightly E.J., Garandi G.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hibert H., Holsappel S., Hags K., Hallo M.F., Itaya M., Jones L.,
RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Ouega B., Park S. H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Boroche B., Rose M., Sadaie Y.,
RA Schiguchi J., Sechwska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Schiguchi A. Tacconi E., Takabachi H., Takabara Y., Takabachi H., Takabara Y.,
RA Schiguchi A., Seror S.J., Serror P., Shin B.S., Soldo B.,
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P37526;
01-OCT-1994
01-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96051385; PubMed=7584024;
Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
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PROSITE; PS00334; MYB 2; 1.

PROSITE; PS50090; MYB 3; 2.

Nuclear protein; DNA-Dinding; Activator; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
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InterPro; IPR001005; Myb_DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98044033; PubMed=9384377;
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S101103; 1POM.
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Tacconi E., Takagi T.,
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MYB 2.
A -> P (IN REF. 2).
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MEDLINE-22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Hypothetical protein; Complete proteome.
SEQUENCE 315 AA; 37978 MW; E9BEZ5481FA13519 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96230334; PubMed=8786100;
Tanaka T., Inazawa J., Nakamura Y
Tanaka T. Inazawa J., Nakamura Y
"Molecular cloning and mapping of
dehydrogenase (MDH1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler B., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F. Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Heart;
Lo A.S.Y., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
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cytoplasmic (EC 1.1.1.37).
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Best Local S
Matches 7
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InterPro; IPR001252; Mdh.
Pfam; PF00056; 1dh; 1.
Pfam; PF02866; 1dh C; 1.
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Q9M714;
01-OCT-2000
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Solanaceae; Petunia.
                                                                                                             "Molecular analysis of the anthocyanin2 in the evolution of flower color."; Plant Cell 11:1433-1444 (1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SI--!- SINILARITY: CONTAINS 2 MYB-LIKE DOMA EMBL; AF146709; AAF66734.1; -...
HSSP, P06876; 1MBK.
                                                                                                                                                                                                                                                     MEDLINE=99380006; Publy Quattrocchio F., Wing Mol J., Koes R.;
                                                        InterPro; IPR001005; Myb_DNA_binding. Pfam; PF00249; myb_DNA-binding; 2. SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=cv. S7; TISSUE=Petal limb;
PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
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Q9qm46 rhizobium 1
Q944983 caenorhabdi
Q44983 caenorhabdi
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Q9qmk7 human immun
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Q8afa4 human immun
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Q8nrt1 corynebacte
Q9fcn7 rhizobium 1
Q8aca6 human immun
Q86646 streptomyce
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Q9q4n2 human immun
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RESULT

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Matches 38
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SMART; SANT; 2.
SMART; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS00090; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 127 AA; 14789 MW; 583D5730
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Q9M721;
01-OCT-2000
01-OCT-2000
01-MAR-2003
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01-MAR-2003
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STRAIN-CV. W22; TISSUE-Petal limb;
STRAIN-CV. W22; PubMed=10449578;
"An der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding; Nuclear protein. SEQUENCE 120 AA; 13935 MW;
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Quattrocchio F., Wing
Mol J., Koes R.;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Solanaceae; Petunia.
                                  NCBI_TaxID=4102;
                                                                                        Petunia hybrida (Petunia).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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HSSP; P06876; 1MBK.
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   SEQUENCE FROM N.A.
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4.8e-32
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4.6e-32;
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                                                                              Query Match
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Matches 38
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                                                                                                                                                                PROSITE; PS00037; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 255 AA; 29007 MW;
                                                                                                                                                                                                                                                                                                                                                                                   in the evolution of flower color.";
Plant Cell 11:1433-1444(1999).
-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol J., Koes R.;
"Molecular analysis of the anthocyanin2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99380006; PubMed=10449578; Quattrocchio F., Wing J., van der Woude K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiids; Solanales; Solanaceae; Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-Binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INCANSFAC; 102955; -. IRANSFAC; 1PRO01005; Myb DNA binding Pfam; PF00249; myb DNA-binding; 2. SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular analysis of the anthocyanin2 in the evolution of flower color."; Plant Cell 11:1433-1444(1999).
                                                                                                                                                                                                                                                                            Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                             EMBL; AF146703; AAF66728.1; HSSP; P06876; 1MBK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. S9; TI:
MEDLINE=99380006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quattrocchio
Mol J., Koes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. V26; TISSUE=Petal limb;
MEDLINE=99380006; PubMed=10449578;
Quattrocchio F., Wing J., van der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petunia integrifolia (Violet-flowered petunia) (Petunia inflata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                       interPro; IPR001005; Myb_DNA_binding
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                                                                                                       Similarity
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                        DEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNT
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(TrEMBLiel.
(TrEMBLiel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Petal limb;
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                                                                              100.0%; E
tive 0;
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15,
23,
                                                                              Score 38; DB; Pred. No. 8.8
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Last annotation update)
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Pred. No
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                                                                                                                                                                      48B18508AFD59C3F CRC64;
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3. 8.8e-32;
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8.8e-32;
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edons; core ev
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                                      109
                                                                                                                       Length 255;
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                                                                                   Indels
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Best Local Similarity
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Q9M718;
01-OCT-2000
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01-MAR-2003
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                                                        "Molecular analysis of the anthocyanin2 in the evolution of flower color."; plant Cell 11:1433-1444(1999).
                                                                                                                                                                                                                                                                  Petunia hybrida (Petunia).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
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-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
-i- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
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STRAIN=CV. W44; TISSUE=Petal.limb;
                 -!- SUBCELLULAR LOCATION: N
-!- SIMILARITY: CONTAINS 2
                                                                                                                      Quattrocchio F., Mol J., Koes R.;
                                                                                                                                                             STRAIN=cv. W115; T
MEDLINE=99380006;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             An2 truncated protein.
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HSSP; P06876; 1MBK.
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MEDLINE=99380006; PubMed=10449578
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llarity 100.0%;
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                                                                                                                                       F., Wing J.,
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                                                                                                                                                               TISSUE=Petal limb; PubMed=10449578;
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14817 MW;
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15,
23,
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23,
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                                     NUCLEAR (BY SIMILARITY)
                   MYB-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Last sequence update)
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Pred. No.
                                                                                                                                              der Woude
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                     DOMAINS
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8.7e-28;
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                                                                                                                                            Souer E.,
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                                                                                                    petunia
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                                                                                                                                              Vetten
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InterPro;

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DNA binding.

HSSP; P06876; 1MBK.

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White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Cteasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Lingin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Lingin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Militscher J., Miranda M., Nguyen M., Niermann W.C., Osborne B.I.,

Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

Wa D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
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Best Local :
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Q9FNV8;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS00334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
                                                                                                                                                                       Nature 408:816-820(2000).

-!- SUBCELLULAR LOCATION: NUCLEAR (E-!- SIMILARITY: CONTAINS 2 WYB-LIKE EMBL; AX008379; AAG38381.1; -- EMBL; AC020665; AAG52160.1; -- HSSP; P06876; 1IDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative transcription factor MYB114 (Myb-related transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00249; myb_DNA-binding; SMART; SM00717; SANT; 2.
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PROSITE; PS00037; MYB_1; 1.
PROSITE; PS00334; MYB_2; 1.
PROSITE; PS50090; MYB_3; 2.
                                                                                     InterPro; IPR001005; Myb DNA binding. Pfam; PF00249; myb DNA-binding; 2. SMART; SM00717; SANT; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "MYB transcription f
Submitted (SEP-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21016719; PubMed=11130712;
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                                                                                                                                                                                                                                                                                                                                                                                     analysis of chromosome 1
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0) to the EMBL/GenBank/DDBJ databases.
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100.0%; Pr
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White-210.6719; PubMed=11130712;

White-O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

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A. Chung M.K., Conn L., Conway A.B., Conway J.-D., Fong B., Fujii C.Y.,

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A. Chung M.K., Conn L., Conway A.B., Conway J.-P., Fong B., Fujii C.Y.,

A. Chung M.K., Conn L., Conway A.B., Khasen N.F., Hughes B., Huizar L.,

A. Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

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B. A. Kim C.J., Tambunga G., Toriumi M.J., Town C.D.,

William J., Wan J., Maranda M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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   Matches
                                                                                                                           Pfam; PF00249; myb DNA-binding; SMAXT; SM00717; SANT; 2. PROSITE; PS00037; MYB 1; 1. PROSITE; PS00334; MYB-2; 1. PROSITE; PS00334; MYB-3; 2. DNA-binding; Nuclear protein. SEQUENCE 246 AA; 28307 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Nuclear protein. SEQUENCE 139 AA; 16007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stracke R., Weisshaar B.; "MYB transcription factor gene nomenclature in Arabidopsis Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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      11.7%; Score 32; DB 100.0%; Pred. No. 2.: ive 0; Mismatches
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100.0%; Pred. No.
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                                                                                                                                  FF1C4B9176040D20 CRC64;
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1.3e-25;
                                DB 10; 1
2.1e-25;
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WEDLINE=21016719; PubMed=11130712;

WA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

A White O., Alonso J., Altati H., Aranjo R., Bowman C.L., Brooks S.Y.,

A White O., Alonso J., Altati H., Aranjo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Fujii C.Y.,

RA Kim C.J., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Milischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Vencer J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
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Q9ZTC3;
01-MAY-1999
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01-MAR-2003 (TrEMBLrel. 23, Last sanotation update)
Putative transcription factor (Production of anthocyanin pigment protein) (MYB-related transcription factor, putative, 65699-67047).
                                                                                                                           -!- SUBCELLULAR LOCATION: NUCLEAR (E

-!- SIMILARITY: CONTAINS 2 MYB-LIKE

EMBL; AF0622915; AAC83637.1; -.

EMBL; AF325124; AAC42002.1; -.

EMBL; AC020665; AAC52164.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYB90 OR PAP2 OR T27F4.14.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
                                                       InterPro; IPR001005; Myb DNA binding. Pfam; PF00249; myb DNA-binding; 2. SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borevitz J.O., Xia Y., Blount J., "Activation Tagging Identifies a Phenylpropanoid Biosynthesis."; Plant Cell 12:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=cv. Columbia-0;
PROSITE; PS00037; MYB_1; PROSITE; PS00334; MYB_2; PROSITE; PS50090; MYB_3;
                                                                                                                                                                                                                                Nature 408:816-820(2000).
                                                                                                                                                                                                                                               thaliana.
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Plant J. 16:263-276(1998).
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MEDLINE=99056848; PubMed=9839469;
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                                                                                                                  HSSP; P06876; 1IDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Columbia;
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01-MAY-1999
01-MAY-1999
01-MAR-2003
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01-OCT-2000
01-MAR-2003
                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                     MYB75
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-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF146704; AAF66729.1; -.
HSSP; P06876; 1MBK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petunia integrifolia (Violet-flowered petunia) (Petunia inflata). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Petunia.
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   SEQUENCE FROM N.A. STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                   Putative transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9ZTC7
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"Molecular analysis of the anthocyanin2 in the evolution of flower color.";
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                                                                                        NCBI_TaxID=3702;
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Pred. No.
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Pred. No.
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3.9e-21
                                                                                                                                                      Embryophyta; Tracheophyta;
edons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Columbia-v;
Borevitz J.O., Xia Y., Blount J.,
"Activation Tagging Identifies a (
Phenylpropanoid Biosynthesis.";
Plant Cell 12:0-0(2000).
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS000314; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear proteit
SEQUENCE 248 AA; 28469 M
                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi.H., Nguyen M., Lam B., Southwick A., Bei, Buehler E., Chin (Chiou J., Choi E., Dunn P., Gonzalez A., Howng B., Kim C., Koo T., Lee J.M., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Pham P., Sakano H., Schwartz J., Shinn P., Thaveri A., Toriumi M., Vaysberg M., Walker M., Yu G., Ecker J., Theologis A., Davis R.W., Yu G., Ecker J., Theologis A., Davis R.W., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.

EMBL; AF325123; AAG42001.1; -.

EMBL; AC009323; AAG09100.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor).

PAPI OR F25p12.92.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00037; MYB 1; 1.
PROSITE; PS000334; MYB 2; 1.
PROSITE; PS50090; MYB 3; 2.
DNA-binding; Nuclear protein.
SEQUENCE 212 AA; 24508 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
- I- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF062908; AAC83630.1; -
- HSSP; P06876; 1IDY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene family from Arabidopsis thaliana."; Plant J. 16:263-276(1998).
                                                                     InterPro; IPR001005; Myb DNA binding. Pfam; PF00249; myb DNA-binding; 2. SMART; SM00717; SANT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Production of anthocyanin pigment 1 protein (Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001005; Myb DNA binding. Pfam; PF00249; myb DNA-binding; 2. SMART; SM00717; SANT; 2.
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01-MAR-2001
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Petroni K., Urzainqui A., Bevan M., Ma
Tonelli C., Paz-Ares J., Weisshaar B.;
                                                                                                                        HSSP; P06876; 1IDY
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Towards functional characterisation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99056848;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Denekamp M., Greco R., Jin H., Leyva Mrzainoui A., Bevan M., Martin C., So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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 28469 MW;
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                protein
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Pred. No.
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 B86103A9AB5CF442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eudicots;
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                                                                                                                                                                                                                                                                 B., Chin C.,
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01-MAR-2003
01-MAR-2003
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Q94FG4;
                      NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
EMBL; AF377306; AAK58019.1; -.
InterPro; IPR001005; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F., "PCR-mediated recombination in a polyploid plant."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                eurosids II; Malvales;
NCBI_TaxID=47615;
                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypioides.
                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-Myb-like transcription factor 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                          Q8H262;
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NON_TER 1
SEQUENCE 179 A
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SEQUENCE
                                                         Plant Mol.
                                                                                   cotton."
                                                                                                                           Cedroni M.L.,
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                        Gossypioides kirkii.
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                                                                                                     "Evolution
                      t Mol. Biol.
; AY115511; A
TER 1
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                                                                                                                                               FROM N.A.
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                                                                                                     and
  181 AA;
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ilarity 100.0%;
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                                                                                                                         Cronn
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                                                                                                     Cronn R.C., expression
                                       AAN28279.1; -.
                                                           0:0-0(2002).
  20967 MW;
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. 23, Last annotation update)
factor Myb 3 (Fragment).
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                                                                                                       MYB
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA70C42F7CC9A8F CRC64;
  OFOA0FDE13250F7D CRC64;
                                                                                                                         K.L.,
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4.5e-20;
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4.5e-18;
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RESULT 15
Q94FG5
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Search completed: January 29, 2004, 20:21:09 Job time : 70 secs
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARI'
-!- SIMILARITY: CONTALNS 2 MYB-LIKE DOMAINS.
EMBL; AF377305; AAKS8018.1; -.
InterPro; IPR001005; Myb DNA binding.
Pfam; PF00249; myb DNA-binding; 2.
SMART; SM00717; SANT; 2.
PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00033; MYB 2; 1.
PROSITE; PS00039; MYB 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Haselkorn T., Osborne C., Wendel J.F.,
PCR-mediated recombination in a polyploid plant.",
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear protein.
NON TER 1
SEQUENCE 184 A/
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Gossypium raimondii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
NCBI_TaxID=29730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q94FG5 PRELIMINARY; PRT; 184 AA.
Q94FG5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myb-like transcription factor Myb 3 (Fragment).
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                                                                                                                                                            67 DLILRLHKLLGNRWSLIAGRLPGRT 91
                                                                                                                                                                                                            75 DLILRLHKLLGNRWSLIAGRLPGRT 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 AA; 21435 MW; FEEDB20F1E3E407A CRC64;
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nilarity 100.0%; Pred. No. 4.6e-18;
Conservative 0; Mismatches 0;
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